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(54) Title: COLLECTION OF PROKARYOTIC DNA FOR TWO HYBRID SYSTEMS HELICOBACTER PYLORI PROTEIN-PROTEIN INTERACTIONS AND APPLICATION THEREOF

(57) Abstract: The present invention concerns collections of recombinant cell clones derived from a prokaryotic genome, more particularly from *Helicobacter pylori* genome, usable for two-hybrid systems and methods to produce such collections. The invention further relates to the identification of *H. pylori* protein-protein interactions and to the application of said collections of recombinant cell clones and said identified proteins interactions to the pharmaceutical and diagnostic field.

AMENDED CLAIMS

[received by the International Bureau on 28 November 2000 (28.11.00); original claim 60 amended; remaining claims unchanged (2 pages)]

b) a polynucleotide having the sequence identified by the reference indicated in the right column "SID®" in table III ;

c) fragment having at least 12 consecutive nucleotides of polynucleotide of a) or b), complement thereof, and RNA corresponding to said polynucleotide ; and

d) a polynucleotide having at least 80 % identity degree after alignment to a nucleic acid sequence of a polynucleotide of a) or b) ;

with the exception of the polynucleotides encoding the polypeptide having the sequence disclosed in the EMBL Data base document Accession number 025045.

61. Purified or isolated polypeptide selected from the group consisting of :

a) a polypeptide having an amino acids sequence identified by the reference indicated in the right column "SID®" in table II, and fragment thereof having at least 5 consecutive amino acids ; and

b) a polypeptide encoded by a polynucleotide according to claim 59 or 60.

62. Use of a polynucleotide according to claim 60 as a primer for amplification.

63. Use of a polynucleotide according to claim 60 as a specific probe for detection.

64. Cloning or expression vector containing a polynucleotide according to anyone of claims 59 and 60.

65. Vector according to claim 64, wherein the vector is the plasmid pACTIIst, pAS2ΔΔ or pP6.

66. Vector according to claim 64, wherein the vector is the plasmid selected from the group consisting of pT25, pKT25, pUT18 and pUT18C.

67. Vector according to claim 64, wherein the vector is self replicated.

68. Vector according to claim 64 or 67, wherein the vector is a viral vector.

69. Vector according to claim 68, wherein the vector is chosen between an adenovirus, AAV, a retrovirus, a proxivirus or an herpes virus.

70. Vector according to anyone of claims 64 to 69 including elements allowing expression and/or secretion of said polynucleotide in a host cell.

71. Host cell transformed with a vector according to anyone of claims 64 to 70.

72. Host cell according to claim 71, wherein the host cell is a prokaryotic cell.

73. Host cell according to claim 71, wherein the host cell is an eukaryotic cell.

74. Method for producing a polypeptide according to anyone of claims 45 and 61, comprising the steps of :

a) cultivating a host cell according to anyone of claims 71 to 73 under conditions and in culture medium allowing the growth of said host cell and the expression of said polypeptide; and

b) recovering said polypeptide directly from the culture medium or from said cultivated cell obtained in step a).

75. Purified or isolated polypeptide obtained by the method according to claim 74.

76. A method for selecting an agent capable of modulating the protein-protein interaction of a step of two polypeptides according to claim 45 comprising the steps of :

a) cultivating a recombinant cell clone containing a reporter gene expression of which is toxic for said recombinant cell clone and transformed with two plasmids wherein :

i) the first plasmid contains a nucleic construct comprising a nucleic sequence encoding a first hybrid polypeptide containing one of said two polypeptides and a DNA binding domain ;

ii) the second plasmid contains a nucleic construct comprising a nucleic sequence encoding a second hybrid polypeptide containing the second of said two polypeptides and an activating domain capable of activating said toxic reporter gene when the first and the second hybrid polypeptides are interacting ;

on a selective medium containing the agent to be tested and allowing the growth of said recombinant cell clone when the toxic reporter gene is not activated ; and

b) selecting agent which is capable of inhibiting the growth of the recombinant cell clone cultivated in step a).

77. A method for selecting an agent capable of modulating the protein-protein interaction of a set of two polypeptides according to claim 45 comprising the steps of :

specific site on the DNA and a domain that is necessary for activation (Keegan et al., 1986, Science, 231(4739): 699-704 Separation of DNA binding from the transcription activating function of eukaryotic regulatory protein).

To date however, the two-hybrid assay system has not been specifically applied to the systematic study of prokaryotic protein-protein interactions although number of diseases are due to prokaryotic microorganisms.

One of the prokaryotic microorganisms presenting a great interest is *Helicobacter pylori*. *Helicobacter pylori* (*H. pylori*) is a microaerophilic, Gram negative, slow growing, spiral shaped and flagellated organism. *H. pylori* has been first isolated in 1983 from gastric biopsy specimen of patient with chronic gastritis (Marshall et al., 1984, Lancet, i:1311-1314, Unidentified curved bacilli in the stomach of patients with gastritis and peptic ulceration).

Helicobacter pylori has become identified as a primary cause of chronic gastroduodenal disorders, such as gastritis, dyspepsia, and peptic ulcers, in humans. Studies have shown (Labigne et al.) that *H. pylori* can be successfully eradicated by a treatment combining two antibiotics with a proton pump inhibitor. However, few antibiotics are active against *H. pylori*, and antibiotic-resistant strains have begun to appear.

H. pylori strain n° 26695 genome has been studied by Tomb et al. (Tomb et al., 1997, Nature, vol. 388, 539-547, The complete genome sequence of the gastric pathogen *Helicobacter pylori*). This strain's genome consists of a circular chromosome with a size of 1,667,867 bp, average G + C content of 39 %, and 1590 predicted coding sequences (open reading frames or "ORF").

The bacterial factors necessary for colonization of the gastric environment, and for virulence of this pathogen, are poorly understood. Examples of known virulence factors are :

- Enzymes involved in neutralizing the acid gastric pH : the multisubunit urease is a characteristic enzyme that is crucial for survival in acidic pH and for successful colonization of the gastric environment, a site that few other microbes can colonize (Labigne et al., WO 93/07273, *Helicobacter pylori* genes necessary for the regulation and maturation of urease, and use thereof). Genes encoding ureases have been located

on a 34 kb chromosome fragment and comprise ureA, ureB, ureC, ureD, ureE, ureF, ureG, ureH and ureI.

- Bacterial flagellar proteins responsible for motility across the mucous layer (Hazell et al., 1986, J. Inf. Dis., 153, 658-663 Campylobacter *pyloridis and gatritis* : association with intracellular spaces and adaptation to an environment of mucus as important factors in colonization of the gastric epithelium; Leying et al., 1992, Mol. Microbiol., 6, 2863-2874 Cloning and genetic characterization of *Helicobacter pylori* flagellin gene) : flagellar filaments biosynthesis comprises A and B flagellins and the filament cap. These two biosyntheses are regulated by flbA gene (Suerbaum et al., French patent application, 1995, N 2 736 360, Cloning and characterization of flbA gene of *Helicobacter pylori*, aflagellated strains production).

- Two other essential toxins for virulence are VacA and CagA :

- VacA is a *H. pylori* toxin that induces the formation of large acidic vacuoles in host epithelial cells. These large vacuoles originate from massive swelling of membranous compartments of late stages of the endocytic pathway (de Bernard et al., 1997, Microbiology, 26(4), 665-674, *Helicobacter pylori* toxin VacA induces vacuole formation by acting in the cell cytosol). Proof for receptor-mediated interaction with VacA has been made by Pagliaccia et al.; m2 allele of vacA gene has always been described as inactive in the in vitro HeLa cell assay, however, the m2 allele is associated with peptic ulcer and is prevalent in populations in which peptic ulcer and gastric cancer have high incidence (Pagliaccia et al., Proc. Natl. Acad. Sci. U.S.A, 1998, 95(17), 10212-10217, The m2 form of the *Helicobacter pylori* cytotoxin has cell type-specific vacuolating activity).

- CagA is one of the proteins encoded by the " cag pathogenicity island " (Spohn et al. 1997, Molecular Microbiology, 26(2), 361-372, Transcriptional analysis of the divergent cagAB genes encoded by the pathogenicity island of *Helicobacter pylori*) found in *H. pylori* strains isolated from most patients with peptic ulcer disease and adenocarcinoma. CagA is produced by 50-60 % of *H. pylori* strains; it is a high molecular weight (120-140 kDa) superficial protein and an immunodominant antigen with unknown function. *H. pylori* strains that produce CagA protein have two genes cagB and cagC (36 and 101 kDa proteins, respectively). These genes are highly

associated with duodenal ulcers (Blaser et al. 1996, WO 96/12825, cagB and cagC genes of *Helicobacter pylori* and related methods and compositions).

- Other virulence factors are : several gastric tissue-specific adhesins (Boren et al., 1993, Science, 262, 1892-1895).

Therapeutic agents are currently available that eradicate *H. pylori* infections *in vitro*. However, methods employing antibiotic agents result in the emergence of bacterial strains which are resistant to these agents.

As number of diseases are due to prokaryotic microorganisms, there is a great need for new tools directed to the functional and global study of these newly characterized complete or partial genome, particurlarly *Escherichia coli* genome, but also of pathogenic microorganisms such as *H. pylori*, *Staphylococcus aureus* and *Streptococcus pneumoniae* genomes.

In addition to the need for these new tools, there is also and especially a need to find new *E. coli*, *H. pylori*, *S. aureus* and *S. pneumoniae* protein-protein interactions for the development of more effective and better targeted therapeutic.

Summary of the invention

The present invention relates to a method for producing a collection of recombinant cell clones usable for two-hybrid systems containing genomic DNA fragments of prokaryotic micro-organism, particularly of *E. coli*, *H. pylori*, *S. aureus* and *S. pneumoniae*, to collection of recombinant cell clones obtainable by this method and kit for screening comprising said collection.

The invention is also directed to a yeast or bacterial two-hybrid system method for identifying a recombinant cell clone expressing a prey polypeptide of a prokaryotic microorganism capable of interacting with a bait polypeptide and a method for identifying said prey polypeptide.

The present invention further comprises polynucleotides or polypeptides corresponding to the prey polypeptides capable of interacting with a bait polypeptide and the protein-protein interactions identified by the yeast or bacterial two-hybrid system method according to the invention, vectors and host cells containing said polynucleotides, and pharmaceutical composition including them.

The present invention also concerns a method for identifying a polynucleotide encoding a selected interacting domain (SID®) of a prey polypeptide of interest from a prokaryotic microorganism capable of interacting with a bait polypeptide.

Another aspect of the present invention relates to a method for selecting an agent capable of modulating the protein-protein interaction identified by the yeast or bacterial two-hybrid system method according to the invention.

Brief description of the drawings

Figure 1 is a restriction map of the plasmid pAS2ΔΔ which may be used for the yeast two-hybrid system.

Figure 2 is a restriction map of the plasmid pACTIIst which may be used for the yeast two-hybrid system.

Figure 3 is a restriction map of the plasmid pUT18 which may be used for the bacterial two-hybrid system. In this figure, each multicloning site (MCS) is detailled.

Figure 4 is a restriction map of the plasmid pUT18C which may be used for the bacterial two-hybrid system. In this figure, each multicloning site (MCS) is detailled.

Figure 5 is a restriction map of the plasmid pT25 which may be used for the bacterial two-hybrid system. In this figure, each multicloning site (MCS) is detailled.

Figure 6 is a restriction map of the plasmid pKT25 which may be used for the bacterial two-hybrid system. In this figure, each multicloning site (MCS) is detailled.

Figure 7 is a schematic representation of the SID® identification method. In this figure, the « Full-length prey protein » is the Open Reading Frame where the identified prey polypeptides are included, the Selected Interaction Domain SID® is determined by comparison of every prey polypeptide fragment.

Figure 8 is a restriction map of the plasmid pP6 which may be used for the yeast two-hybrid system.

Detailed description of the invention

The present invention is directed to a method for producing a collection of recombinant cell clones usable for two-hybrid systems comprising the steps of :

a) fragmenting DNA ;

b) inserting polynucleotidic fragments obtained in step a) in plasmids in such a way that the expression of said plasmids in host cell leads to an hybrid polypeptide containing a specific domain capable of activating a reporter gene when associated with a complementary domain ;

c) transforming cell clones with plasmids obtained in step b); and

d) optionally, selecting the transformed recombinant cell clones obtained in step c) ;

wherein DNA of step a) is genomic DNA obtained from a prokaryotic micro-organism.

The step a) of fragmenting DNA according to the method of the invention may be obtained by enzyme digestion, sonication or nebulization of the source of genomic DNA, sonication and nebulization ensuring a random cleavage of the starting DNA material and thus an excellent representation of all the possible inserts.

In a preferred embodiment, the step a) of fragmenting DNA of the method according to the invention is carried out by a nebulization process, for example, with a commercial nebulizer (GATC).

In a preferred embodiment, the plasmid used in the method for producing a collection of recombinant cell clones usable for two-hybrid systems according to the present invention may comprise in addition a nucleic sequence encoding a promoter, a multicloning site, a terminator site and a selection marker, operably linked.

A "promoter" refers to a DNA sequence recognized by the transcriptional machinery of the cell required to initiate the specific transcription of a gene.

A sequence which is "operably linked" to a regulatory sequence such as a promoter means that said regulatory element is in the correct location and orientation in relation to the nucleic acid to control RNA polymerase initiation and expression of the nucleic acid of interest. As used herein, the term "operably linked" refers to a linkage of polynucleotide elements in a functional relationship. For instance, a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the coding sequence. More precisely, two DNA molecules (such as a polynucleotide containing a promoter region and a polynucleotide encoding a desired polypeptide or polynucleotide) are said to be "operably linked" if the nature of the linkage between the two polynucleotides does not (1) result in the introduction of a frame-shift mutation or (2) interfere with the ability of the polynucleotide containing the promoter to direct the transcription of the coding polynucleotide.

As a promoter, one could use full or truncated ADH promoter.

By specific domain, it is intended a domain whose association with a complementary domain leads to the activation of a reporter gene.

In one particular embodiment of this invention, the specific domain may be a transcriptional activating domain or a DNA-binding domain and the complementary domain may, respectively, be a DNA binding domain or a transcriptional activation domain.

Transcriptional activating domain and DNA-binding domain may be derived from Gal4 and LexA respectively.

In another particular embodiment of the invention, the activation domain is a part of an enzyme and the complementary domain is the other part of the same enzyme. Proximity of the two parts of the enzyme may restore the enzyme activity and activate a reporter gene.

For example, specific and complementary domain may be T25 and T18 polypeptides that constitute the catalytic domain of *Bordetella pertussis* adenylate cyclase.

The reporter gene may be contained either in a plasmid of recombinant cell clone or in its genome.

As an illustrative embodiment of the invention, the reporter gene is chosen among the group consisting in a nutritional gene or also a gene the expression of which is visualized by colorimetry such as His3, LacZ or both LacZ and His3.

As a selective marker, gene encoding for a toxin, color marker of the type of the Green Fluorescent Protein (GFP), gene encoding for phage receptor proteins or fragment thereof such as phage λ receptor lam B and any other gene giving selectable phenotype, resistance gene, such as ampicilline, kanamycin, tetracyclin or lactose or maltose nutritional gene, may be used.

In a particularly preferred embodiment, the invention relates to a method according to the invention wherein DNA of step a) is genomic DNA obtained from *Helicobacter pylori* (see example 1.A.), *Escherichia coli*, *Staphylococcus aureus* and *Streptococcus pneumoniae*.

The invention also concerns a collection of recombinant cell clones usable for two-hybrid systems obtainable by a method according to the invention.

The invention further concerns a collection of recombinant cell clones usable for two-hybrid systems, each recombinant cell clone containing a polynucleotide inserted in a plasmid whose expression leads to hybrid polypeptide containing a specific domain, wherein the said polynucleotide is a genomic DNA fragment obtained from a prokaryotic micro-organism.

In a preferred embodiment, said genomic DNA fragment is obtained by a fragmentation process by nebulization.

In a particularly preferred embodiment, the invention relates to collection of recombinant cell clones of the invention wherein the prokaryotic micro-organism is *Helicobacter pylori*, *Escherichia coli*, *Staphylococcus aureus* and *Streptococcus pneumoniae*.

The present invention also comprises a collection of recombinant cell clones according to the invention, wherein the recombinant cell clones are selected from the group consisting of Gram+ or Gram- bacteria, yeasts, fungi and mammalian cells, particularly from the group consisting of *Escherichia coli* bacteria and *Saccharomyces cerevisiae* yeast.

The present invention further concerns a collection of recombinant cell clones according to the invention, wherein the plasmids comprise at least a nucleic sequence coding a promoter, a specific domain, a multicloning site where the said polypeptide is cloned, and a selection marker.

In a preferred embodiment, the present invention further concerns a collection of recombinant cell clones according to the invention, wherein the polynucleotide is inserted in the plasmid pACTIIst or in the plasmid pP6.

In a more preferred embodiment, the present invention further concerns a collection of recombinant cell clones according to the invention, wherein the collection contains 10^6 to 10^7 or to 10^8 recombinant *Escherichia coli* clones and wherein the proportion of independent cell clones with insert is at least 60 %, 70 %, 80 %, 90 %, 95 % or 97 %.

The present invention particularly comprises the collection of recombinant cell clones according to the invention which has been deposited in the Collection National de Cultures de Microorganismes (CNCM) (France, Paris) on April 13, 1999 under the

accession number I-2181, and on March 23, 2000 under the accession numbers I-2416, I-2414, I-2415 and I-2417.

The collection of recombinant cell clones which has been deposited under the accession number I-2181 (identification reference : HGXBHP1) concerns a genomic librairy of *Helicobacter pylori* 26695 strain, cloned in the stop bis pACTII vector, transformed in *Escherichia coli* DH10B. The collection contains about 10^7 independent clones with an insert pourcentage of about 97 % and an insert average size of 1000 pb.

The collection of recombinant cell clones which has been deposited under the accession number I-2416 (identification reference : HGXBSA1) concerns a genomic librairy of *Staphylococcus aureus* col strain, cloned in the pP6 vector, transformed in *Escherichia coli* DH10B. The collection contains about 6.8 10^7 independent clones with an insert pourcentage superior to 95 % and an insert average size of 1100 pb.

The collection of recombinant cell clones which has been deposited under the accession number I-2415 (identification reference : HGXBEC1) concerns a genomic librairy of *Escherichia coli* MG1655 strain, cloned in the pP6 vector, transformed in *Escherichia coli* DH10B. The collection contains about 3 10^7 independent clones with an insert pourcentage superior to 98 % and an insert average size of 853 pb.

The collection of recombinant cell clones which has been deposited under the accession number I-2417 (identification reference : HGXBHP4) concerns a genomic librairy of *Helicobacter pylori* 26695 strain, cloned in the pP6 vector, transformed in *Escherichia coli* DH10B. The collection contains about 1.9 10^7 independent clones with an insert pourcentage superior to 98 % and an insert average size of 1009 pb.

In another aspect, the present invention relates to a collection of recombinant cell clones according to the invention, wherein the collection contains 10^5 to 1.5 x 10^7 haploid recombinant *Saccharomyces cerevisiae* clones and wherein the proportion of independant cell clones with insert is at least 60 %, 70 %, 80 %, 90 %, 95 % or 97 %.

The present invention particularly comprises the collection of recombinant cell clones according to the invention which has been deposited in the Collection National de Cultures de Microorganismes (CNCM) on April 13, 1999 under the accession

number I-2182, and on March 23, 2000 under the accession numbers I-2420, I-2419 and I-2418.

The collection of recombinant cell clones which has been deposited under the accession number I-2182 (identification reference : HGXYHP1) concerns a genomic librairy of *Helicobacter pylori*, 26195 strain, which has been amplified in *E. coli* (HGXBHP1 librairy), cloned in the stop bis pACTII vector, transformed in *Saccharomyces cerevisiae*, Y187 strain, and containing about 2 10^6 independent clones.

The collection of recombinant cell clones which has been deposited under the accession number I-2420 (identification reference : Lib Sa2) concerns a genomic librairy of *Staphylococcus aureus*, col strain, which has been amplified in *E. coli* (HGXBSA1 librairy), cloned in the pP6 vector, transformed in *Saccharomyces cerevisiae*, Y187 strain, containing about 2.2 10^6 independent clones, and a cell concentration about 5 10^8 cells/ml.

The collection of recombinant cell clones which has been deposited under the accession number I-2419 (identification reference : Sp in Y187 pP6) concerns a genomic librairy of *Streptococcus pneumoniae*, type 4 strain, which has been amplified in *E. coli* (HGXBSP1 librairy), cloned in the pP6 vector, transformed in *Saccharomyces cerevisiae*, Y187 strain, containing about 2.8 10^6 independent clones, and a cell concentration about 5 10^8 cells/ml.

The collection of recombinant cell clones which has been deposited under the accession number I-2418 (identification reference : E.coli in Y187 lib1) concerns a genomic librairy of *Escherichia coli*, MG1655 strain, which has been amplified in *E. coli* (HGXBEC1 librairy), cloned in the pP6 vector, transformed in *Saccharomyces cerevisiae*, Y187 strain, containing about 4 10^6 independent clones, and a cell concentration about 5 10^8 cells/ml.

In another aspect, the present invention relates to a collection of recombinant cell clones according to the invention, wherein the polynucleotide is inserted in the plasmid pAS2ΔΔ.

Still another aspect, the present invention relates to a collection of recombinant cell clones according to the invention, wherein the polynucleotide is inserted in a plasmid selected from the group consisting of pT25, pKT25, pUT18 and pUT18C.

The present invention also relates to a kit for screening protein-protein interaction comprising a collection of recombinant cell clones usable for two-hybrid systems according to the invention.

In a particular embodiment of the collection according to the invention, the DNA library is presented as a ready to use kit for screening protein-protein interaction consisting in a collection of recombinant haploid yeast cells containing the whole genome as inserts generated during the construction of the DNA library under the form of prey polynucleotides, said collection of yeast cells being frozen in multiple vial containing an identical biological material.

The present invention also provides a generally method for selecting a polynucleotide of the collection according to the present invention, encoding a prey polypeptide, that is capable of interacting with bait polypeptide of interest.

As used interchangeably herein, the terms "polynucleotides", "nucleic acid" "oligonucleotides", include RNA, DNA, or RNA/DNA hybrid sequences of more than one nucleotide in either single chain or duplex form. The polynucleotide sequences of the invention may be prepared by any known method, including synthetic, recombinant, ex vivo generation, or a combination thereof, as well as utilizing any purification methods known in the art.

The term "purified" is used herein to describe a polynucleotide of the invention which has been separated from other compounds including, but not limited to other nucleic acids, carbohydrates, lipids and proteins. A polynucleotide is substantially pure when at least about 50 %, preferably 60 to 90 % weight/weight of a sample exhibits a single polynucleotide sequence, more usually about 95 %, and preferably is over about 99 %.

As used herein, the term "isolated" requires that the material be removed from its original environment (e.g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or DNA or polypeptide, separated from some or all of the coexisting materials in the natural system, is isolated. Such

polynucleotide could be part of a vector and/or such polynucleotide or polypeptide could be part of a composition, and still be isolated in that the vector or composition is not part of its natural environment.

The term "polypeptide" refers to a polymer of amino acids without regard to the length of the polymer ; thus, peptides, oligopeptides, and proteins are included within the definition of polypeptide, theses terms as used herein are interchangeable. The term "polypeptide" also does not specify or exclude post-expression modifications of polypeptides, for example, polypeptides which include the covalent attachment of glycosyl groups, acetyl groups, phosphate groups, lipid groups and the like are expressly encompassed by the term polypeptide. Also included within the definition are polypeptides which contain one or more analogs of an amino acid (including, for example, non-naturally occurring amino acids, amino acids which only occur naturally in an unrelated biological system, modified amino acids from mammalian).

The term "purified" is used herein to describe a polypeptide of the invention which has been separated from other compounds including, but not limited to nucleic acids, carbohydrates, lipids and other proteins. A purified polypeptide typically comprises about 50 %, preferably 60 to 90 % weight/weight of a protein sample, more usually about 95 %, and preferably is over about 99 % pure.

Bait polypeptide of interest is either a prokaryotic polypeptide encoded by a polynucleotide of the collection according to the present invention, or any other polypeptides of interest. Other polypeptides of interest can be polypeptides of an organism that may be infected by the prokaryotic micro-organism, for example, mammalian organism, in particular human organism.

The following described method is the mating yeast two-hybrid system and the bacterial two-hybrid system but variants of two-hybrid systems could also be used.

For example, the three hybrid system (Tirode et al., 1997, Journal of Biological Chemistry, 272, 22995-22999, A conditionally expressed third partner stabilises or prevents the formation of a transcriptional activator in a three-hybrid system) involves three polypeptides that allow or prevent the formation of the transcriptional activator. Beside the two-hybrid fusion proteins, the third partner is under the control of the Met25 promoter, which is positively regulated in medium lacking methionine. Another variant is the reverse two-hybrid system (Vidal et al., 1996, Proc. Natl. Sci., 93, 10315-

10320, Reverse two-hybrid and one-hybrid system to detect dissociation of protein-protein and DNA-protein interaction) where a collection of molecules can be screened that may inhibit a specific protein-protein interaction.

Yet another aspect, the present invention relates to yeast two-hybrid system method for identifying a recombinant cell clone containing a prey polynucleotide encoding a prey polypeptide capable of interacting with a bait polypeptide comprising the steps of :

a) mating at least one first haploid recombinant cell clone of a collection of recombinant cell clones according to the invention transformed with a plasmid containing the prey polynucleotide to be assayed with a second haploid recombinant *S. cerevisiae* cell clone transformed with a plasmid containing a bait polynucleotide encoding said bait polypeptide ;

b) cultivating diploid cell obtained in step a) on selective medium; and

c) selecting recombinant cell clones capable of growing on selective medium.

In a particular embodiment, the invention is directed to a yeast two-hybrid system method for identifying a prey polynucleotide encoding a prey polypeptide capable of interacting with a bait polypeptide comprising the steps of :

a) identifying a recombinant cell clone containing a prey polynucleotide encoding a prey polypeptide capable of interacting with a bait polypeptide according to the invention ; and

b) characterizing the prey polynucleotide contained in each recombinant cell clone selected in step a).

By yeast two-hybrid system is intended a method that usually makes use of at least one reporter gene, the transcription of which is activated when a prey polypeptide and a bait polypeptide produced by recombinant cell, due to the triggering of the transcription of said at least one reporter gene when both the specific domain contained in one prey polypeptide and the complementary domain contained in the bait polypeptide are in proximity one to the other. In an advantageous variant of yeast two hybrid system, prey polynucleotides encoding for prey polypeptides and bait polynucleotides encoding for bait polypeptides or proteins are inserted in recombinant haploid yeast cells, then a mating step leads to diploid yeast cells that produce the prey polypeptide and the bait polypeptide.

By at least one reporter gene according to the invention, it is intended from one to five, and preferably two or three reporter genes, the transcription of which is activated within the recombinant diploid yeast cell when the encoded bait and prey polypeptide are capable of interacting.

Preferably, the at least one reporter gene is contained in the first recombinant haploid yeast cell containing the bait polynucleotide.

The at least one reporter gene may be contained either in a plasmid of the recombinant diploid yeast cell or in its genome.

As an illustrative embodiment, the at least one reporter gene is located in the chromosome of one recombinant haploid yeast cell used according to the previously described two-hybrid system and preferably the yeast cell containing the bait polynucleotide. The at least one reporter gene can be chosen among the group consisting in a nutritional gene or also a gene the expression of which is visualized by colorimetry, such as His3, LacZ or both LacZ and His3.

By " prey polynucleotide ", it is intended a chimeric polynucleotide encoding a chimeric polypeptide comprising i) a specific domain and ii) a polypeptide that is to be tested for interaction with a bait polypeptide. The specific domain is preferably a transcriptional activating domain.

The prey polynucleotide may be obtained from a genomic library of a prokaryotic micro-organism, preferably from genomic DNA of *Helicobacter pylori*.

By a " bait polynucleotide ", it is intended a chimeric polynucleotide encoding a chimeric polypeptide comprising i) a complementary domain and ii) a polypeptide that is to be tested for interaction with at least one prey polypeptide. The complementary domain is preferably a DNA-binding domain that recognizes a binding site on a detectable gene that is contained in a host organism.

Using as the bait polynucleotide, a complete open reading frame (ORF) that may be obtained either by digestion with a restriction endonuclease (Sambrook et al., 1973, Biochemistry 12(16): 3055-63 *Detection of two restriction endonuclease activities in Haemophilus parainfluenzae using analytical agarose-ethidium bromide electrophoresis*) or by digestion with an exonuclease such as Ball, or also by DNA synthesis. The complete ORF can also correspond to a given prey selected at given round with a two-hybrid system. An " open reading frame ", also referred to herein as

ORF, is a region of nucleic acid which encodes a polypeptide. This region may represent a portion of a coding sequence or a total sequence and be determined from a stop to stop codon or from a start to stop codon.

" DNA-binding domain " refers to a protein that specifically interacts with desoxyribonucleotide strands. A sequence-specific DNA binding protein binds to a specific sequence or family of specific sequences showing a high degree of sequence identity with each other.

The DNA binding domain of the bait polypeptide and the transcriptional activating domain of the prey polypeptide may be of different kinds. As an illustrative embodiment, these can be derived from LexA or also Gal4.

In one particular experiment of the yeast two-hybrid system, prey polypeptides are encoded by prey polynucleotides cloned in plasmid pACTIIst carrying Leu2 selection gene transformed in Y187 yeast cells carrying leucine auxotrophy and bait polypeptide are encoded by bait polynucleotide cloned in plasmid pAS2ΔΔ carrying Trp1 selection gene transformed in CG1945 yeast cells carrying tryptophane auxotrophy.

In another aspect, the present invention relates to a bacterial two-hybrid system method for identifying a recombinant cell clone containing a prey polynucleotide encoding a prey polypeptide capable of interacting with a bait polypeptide comprising the steps of :

a) transforming bacterial cell clones with a plasmid containing a bait polynucleotide encoding said bait polypeptide ;

b) rescuing prey plasmids containing prey polynucleotides from the collection according to the present invention ;

c) transforming the recombinant bacterial cell clones obtained in step a) with the plasmid rescued in step b) ;

d) cultivating bacterial recombinant cells obtained in step c) on selective medium ;

e) selecting recombinant cell clones capable of growing on selective medium.c) selecting recombinant cell clones capable of growing on selective medium.

In a preferred embodiment, the preparation of bacterial recombinant cells obtained in step c) of the bacterial two-hybrid system method for identifying a recombinant cell clone according to the invention comprises the following steps :

1) *E. coli* is firstly transformed with bait plamid (standard protocol with chimio- or electro-competent cells) ;

2) prey plasmids are rescued from collection according to the invention (prey plasmids are in *E. coli* bacterial strain, cf. protocol 1.B « the plasmid DNA contained in E. coli are extracted (Qiagen) from aloquoted E. coli frozen cells ») ;

3) rescued prey plasmids are then transformed in recombinant *E coli* of step 1 according to standard protocols of transformation (for example using electro- of chimio-competent cells).

In a particular embodiment, the invention is directed to a bacterial two-hybrid system method for identifying a prey polynucleotide encoding a prey polypeptide capable of interacting with a bait polypeptide comprising the steps of :

a) identifying a recombinant cell clone containing a prey polynucleotide encoding a prey polypeptide capable of interacting with a bait polypeptide according to the invention ; and

b) characterizing the prey polynucleotide contained in each recombinant cell clone selected in step a).

By bacterial two-hybrid system is intended a method that usually makes use of at least one reporter gene, the transcription of which is activated when a prey polypeptide and a bait polypeptide produced by recombinant cell, due to the triggering of the transcription of said at least one reporter gene when both the specific domain contained in one prey polypeptide and the complementary domain contained in the bait polypeptide are in proximity one to the other.

In a particular embodiment of the bacterial two-hybrid system, specific domain of prey polypeptide and complementary domain of bait polypeptide are part of the catalytic domain of an enzyme. Interaction of prey polypeptide and bait polypeptide allows restoration of enzyme catalytic domain and, as a consequence, to the restoration of the enzyme activity.

In a more preferred embodiment of the bacterial two-hybrid method, enzyme is Bordetella *pertussis* adenylate cyclase which activation, via proximity of T25 and T18 fragments of the catabolic domain, leads to cAMP synthesis, cAMP then triggers transcriptional activation of catabolic operons, such as lactose or maltose.

Still another aspect, the present invention relates to a method according to the invention, wherein the bait polypeptide and the prey polypeptide (encoded by a polynucleotide inserted in cell clone from the collection according to the present invention) are originating from the same prokaryotic micro-organism, particularly from *Helicobacter pylori*, *Escherichia coli*, *Staphylococcus aureus* or *Streptococcus pneumoniae* or wherein the bait polypeptide is originating from a human polypeptide and the prey polypeptide is originating from a prokaryotic micro-organism, particularly from *Helicobacter pylori*.

Yet another aspect, the present invention relates to a recombinant diploid yeast cell obtained by step a) of the yeast two-hybrid system method for identifying a recombinant cell clone according to the invention as described above.

The recombinant diploid yeast cell obtained by the the yeast two-hybrid system method for identifying a recombinant cell clone according to the invention, also forms part of the present invention.

By performing yeast or bacterial two-hybrid system, it can be possible to identify for one particular bait interacting prey polypeptide. Prey polynucleotide that has been selected by testing the collection in a screening two-hybrid method encodes for polypeptide interacting with a protein of interest.

The running of the two-hybrid method leads to the identification of interactions between prokaryotic- prokaryotic polypeptides, especially *Helicobacter pylori*, *Escherichia coli*, *Staphylococcus aureus* or *Streptococcus pneumoniae* polypeptides, or eukaryotic-prokaryotic polypeptides, these interactions are also part of the invention.

In another aspect, the present invention is directed to a polynucleotide, or fragment thereof, encoding a prey polypeptide capable of interacting with a bait polypeptide wherein said polynucleotide is identified by a method according to the invention.

In a preferred embodiment, the invention comprises the polynucleotides according to the invention, selected from the group consisting of :

a) a polynucleotide having the nucleic acid sequence of an ORF identified by the reference indicated in the right column "interacting ORF" in table I, and fragment thereof having at least 12 consecutive nucleotides ;

b) a polynucleotide having at least 80 %, preferably at least 85 %, 90 %, 95 % and 99 %, nucleotides identity degree after alignment to a nucleic acid sequence of a polynucleotide of a) ;

c) a polynucleotide comprising the nucleic acid sequence of a polynucleotide of a) or b).

Still another aspect, the present invention is directed to a polynucleotide, or fragment thereof, encoding a bait polypeptide capable of interacting with a prey polypeptide wherein the polynucleotide encoding said prey polypeptide is identified by a method according to the invention.

In a preferred embodiment, the invention comprises the polynucleotides according to the invention, selected from the group consisting of :

a) a polynucleotide having the nucleic acid sequence of an ORF identified by the reference indicated in the left column "bait polypeptide" in table I, and fragment thereof having at least 12 consecutive nucleotides ;

b) a polynucleotide having at least 80 %, preferably at least 85 %, 90 %, 95 % and 99 %, identity degree after alignment to a nucleic acid sequence of a polynucleotide of a) ;

c) a polynucleotide comprising the nucleic acid sequence of a polynucleotide of a) or b).

Yet another aspect, the present invention relates to a set of two polynucleotides consisting of a first polynucleotide, or fragment thereof, encoding a prey polypeptide capable of interacting with a bait polypeptide according to the invention and a second polynucleotide, or a fragment thereof having at least 12 consecutive nucleotides, encoding said bait polypeptide.

The polypeptides encoded by the polynucleotides according to the invention and the sets of two polypeptides encoded by the sets of two polynucleotides according to the invention, also form part of the invention.

In a preferred embodiment, the invention concerns an isolated complex comprising at least the two polypeptides encoded by a set of two polynucleotides according to the invention, preferably said two polypeptides are associated in the complex by affinity binding.

In a preferred embodiment, the invention concerns an isolated complex comprising at least a polypeptide encoded by the ORF HP1198 (or a fragment thereof, preferably one of its SID® domains, or homologuous polypeptide thereof exhibiting at least 80 % identity degree) and a polypeptide encoded by the ORF HP1293 (or a fragment thereof, preferably one of its SID® domains, or homologuous polypeptide thereof exhibiting at least 80 % identity degree).

In a preferred embodiment, the invention concerns an isolated complex comprising at least a polypeptide encoded by the ORF HP1198 (or a fragment thereof, preferably one of its SID® domains, or homologuous polypeptide thereof exhibiting at least 80 % identity degree) and a polypeptide encoded by the ORF HP0088 (or a fragment thereof, preferably one of its SID® domains, or homologuous polypeptide thereof exhibiting at least 80 % identity degree).

In a preferred embodiment, the invention concerns an isolated complex comprising at least a polypeptide encoded by the ORF HP1198 (or a fragment thereof, preferably one of its SID® domains, or homologuous polypeptide thereof exhibiting at least 80 % identity degree) and a polypeptide encoded by the ORF HP1032 (or a fragment thereof, preferably one of its SID® domains, or homologuous polypeptide thereof exhibiting at least 80 % identity degree).

In another aspect, the present invention relates to a protein-protein interaction wherein the two interacting proteins consist of a set of two polypeptides according to the invention.

In a preferred embodiment, the invention relates to the protein-protein interactions according to the invention, wherein the sets of two polypeptides consist of two *Helicobacter pylori*, *Escherichia coli*, *Staphylococcus aureus* or *Streptococcus pneumoniae* polypeptides.

When several reiterations of the two-hybrid method are performed and thus common bait and prey polypeptide are selected, a map of all the interactions between these polypeptides may be designed, that take into account of the known and/or suspected biological function of each of the interacting polypeptides.

Such an Proteins Interaction Map (PIM®) may help the one skilled in the art to decipher a whole metabolical and/or physiological pathway that is functionally active

within the host organism from which the initial DNA library is derived. Protein Interaction Map and computable version of PIM® are part of the present invention.

Therefore still another aspect, the present invention is directed to a computable readable medium (such as floppy disk, diskette, CD-rom, and all electronic or magnetic format which can be read by a computer) having stored thereon protein-protein interactions according to the invention, preferably stored in a form of a protein interaction map, as showed, for example, in Fromont-Racine et al., Nature Genetics, 1997, Letter, 277-281, figure 3, page 279.

In a preferred embodiment, the invention comprises a computable readable medium according to the invention, wherein the protein-protein interactions stored thereon are linked to annotated database, for example through Internet.

In an other preferred embodiment, the invention comprises a data bank containing the protein-protein interactions stored thereon, said databank being avalaible on a World-Wide Web site, said databank may be annoted by means of others databank.

As the source genomic DNA is randomly fragmented before being inserted in recombinant vectors, several prey polypeptides may be selected for one bait polypeptide. Therefore it is possible to define the Selected Interacting Domain (SID®) which contains the precise polypeptide domain involved in the interaction between the prey polypeptide and the bait polypeptide.

So, in another aspect, the invention relates to a method for identifying a polynucleotide encoding a selected interacting domain (SID®) of a prey polypeptide of interest from a prokaryotic micro-organism capable of interacting with a bait polypeptide comprising the steps of :

a) selecting from prey polynucleotides identifying by a method according to the invention all prey polynucleotides encoding a polypeptide capable of interacting with said bait polypeptide and containing a nucleic acid fragment identical to a nucleic fragment of the polynucleotide encoding the prey polypeptide of interest ;

b) determining the polynucleotide common to said all prey polynucleotides selected in step a); and

c) identifying the polynucleotide determining in step b) as being the polynucleotide encoding the selected interacting domain (SID®) of said prey polypeptide of interest.

The polynucleotides encoding a selected interacting domain (SID®) of a prey polypeptide of interest from a prokaryotic micro-organism capable of interacting with a bait polypeptide obtainable by this method, also form part of the invention.

In a particular embodiment, the prey polypeptide of interest is originating from *Helicobacter pylori*, *Escherichia coli*, *Staphylococcus aureus* or *Streptococcus pneumoniae*.

In a preferred embodiment, the polynucleotides encoding a selected interacting domain (SID®) of a prey polypeptide of interest according to the invention are selected from the group consisting of :

a) a polynucleotide encoding an amino acids sequence identified by the reference indicated in the right column " SID®" in table II ;

b) a polynucleotide having the sequence identified by the reference indicated in the right column " SID®" in table III ;

c) fragment having at least 12, 15, 25 or 50 consecutive nucleotides of polynucleotide of a) or b), complement thereof, and RNA corresponding to said polynucleotide ; and

d) a polynucleotide having at least 80 %, preferably 85 %, 90 %, 95 % and 99 %, identity degree after alignment to a nucleic acid sequence of a polynucleotide of a) or b).

The term "complement thereof" are used herein to refer to the sequences of polynucleotides which is capable of forming Watson & Crick base pairing with another specified polynucleotide throughout the entirety of the complementary region. This term is applied to pairs of polynucleotides based solely upon their sequences and not any particular set of conditions under which the two polynucleotides would actually bind.

The term "degree of sequence identity" is used herein to refer to comparisons among polynucleotides and polypeptides, and are determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of

positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. Homology is evaluated using any of the variety of sequence comparison algorithms and programs known in the art. Such algorithms and programs include, but are by no means limited to BLASTN, BLASTP (Altschul et al., 1990, J. Mol. Biol. 215(3): 403-410 / Altschul et al., 1993, Nature Genetics 3:266-272 / Altschul et al., 1997, Nuc. Acids Res. 25:3389-3402).

The definition of sequence identity given above is the definition that would use one of skill in the art. The definition by itself does not need the help of any algorithm, said algorithms being helpful only to achieve the optimal alignments of sequences, rather than the calculation of sequence identity.

From the definition given above, it follows that there is a well defined and only one value for the sequence identity between two compared sequences which value corresponds to the value obtained for the best or optimal alignement.

In the BLAST N or BLAST P "BLAST 2 sequence" (Tatusova et al., *Blast 2 sequences - a new tool for comparing protein and nucleotide sequences*, FEMS Microbiol. Lett. 174 : 247-250) software which is available in the web site http://www.ncbi.nlm.nih.gov/gorf/bl2.html, and habitually used by the inventors and in general by the skilled man for comparing and determining the identity between two sequences, the "open gap penaltie" and « extension gap penaltie » parameters which depend on the substitution matrix selected regarding the nature and the length of the sequence to be compared are directly selected by the software (i.e "5" and "2" respectively for substitution matrix BLOSUM-62). The identity percentage between the two sequences to be compared is directly calculated by the software.

In another object, the invention also comprises the polypeptides selected from the group consisting of :

a) a polypeptide having an amino acids sequence identified by the reference indicated in the right column "SID®" in table II, and fragment thereof having at least 5 consecutive amino acids ; and

b) a polypeptide encoded by a polynucleotide encoding a selected interacting domain (SID®) of a prey polypeptide of interest according to the invention.

Still another aspect, the invention relates to the use of a polynucleotide according to the present invention as a primer or a probe for the amplification and/or the

detection of polynucleotide encoded a prey polypeptide of interest, or its SID®, capable of interacting with a bait polypeptide according to the present invention.

In another aspect, the present invention concerns cloning or expression vector containing a polynucleotide according to the invention.

Particularly preferred vectors of the invention include the plasmid pACTIIst, pAS2ΔΔ, pP6 or the plasmid selected from the group consisting of pT25, pKT25, pUT18 and pUT18C.

Further preferred vectors are self replicated or viral vectors, such as adenovirus, AAV, a retrovirus, a poxvirus or an herpes virus.

The vectors according to the invention, characterized in that they comprise the elements allowing the expression and/or the secretion of the said sequences in a host cell, also form part of the invention.

Vector according to the invention including elements allowing expression and/or secretion of said polynucleotide in a host cell also form part of the invention.

The vectors according to the invention characterized in that they comprise a promoter and/or regulator sequence, or a sequence for cellular addressing according to the invention, or one of their fragments, are also included in the invention.

The said vectors will preferably comprise a promoter, signals for initiation and termination of translation, as well as appropriate regions for regulation of transcription. They may also be capable of being stably maintained in the cell and may optionally possess particular signals specifying the secretion of the translated protein.

These different control signals are chosen according to the cellular host used. To this end, the nucleic acid sequences according to the invention may be inserted into autonomously replicating vectors inside the chosen host, or integrative vectors of the chosen host.

Among the autonomously or self replicating systems, there will be preferably used according to the host cell, systems of the plasmid or viral type, it being possible for the viral vectors to be in particular adenoviruses (Perricaudet et al., 1992, La Recherche 23 : 471-473, 1992), retroviruses, poxviruses or herpes viruses (Epstein et al., 1992, Médecine/Sciences 8 : 902-911, 1992). Persons skilled in the art know the technologies which can be used for each of these systems.

When the integration of the sequence into the chromosomes of the host cell is desired, it will be possible to use, for example, systems of the plasmid or viral type ; such viruses will be, for example, retroviruses (Temin, 1986, In Kucherlapati R., ed. Gene Transfer, New York, Plenum Press, 149-187, 1986), or AAVs (Carter, 1993, *Curr. Op. Biotechnology* **3** : 533-539, 1993).

Such vectors will be prepared according to the methods commonly used by persons skilled in the art, and the clones resulting therefrom may be introduced into an appropriate host by standard methods such as, for example, lipofection, electroporation or heat shock.

The invention comprises, in addition, the host cells, in particular eukaryotic and prokaryotic cells, transformed by the vectors according to the invention.

Among the cells which can be used for these purposes, there may of course be mentioned bacterial cells (Olins et al., Curr. Op. Biotechnology 4 : 520-525, 1993), but also yeast cells (Buckholz, Curr. Op. Biotechnology 4 : 538-542, 1993), as well as animal cells, in particular mammalian cell cultures (Edwards and Aruffo, Curr. Op. Biotechnology 4 : 558-563, 1993), and in particular Chinese hamster ovary cells (CHO), but also insect cells in which it is possible to use methods using baculoviruses, for example (Luckow et al., Curr. Op. Biotechnology 4 : 564-572, 1993). A preferred cellular host for the expression of the proteins of the invention consists of the CHO cells.

The cells according to the invention can be used in a method for the production of a polypeptide according to the invention, as described below, and can also serve as a model for analysis and screening.

So, the present invention comprises a method for producing a polypeptide of the invention comprising the steps of :

a) cultivating a host cell according to the invention under conditions and in culture medium allowing the growth of said host cell and the expression of said polypeptide ; and

b) recovering said polypeptide directly from the culture medium or from said cultivated cell obtained in step a).

Recombinant polypeptide obtained by the method above also form part of the invention.

The term "recombinant polypeptide" is used herein to refer to polypeptides that have been artificially designed and which comprise at least two polypeptide sequences that are not found as contiguous polypeptide sequences in their initial natural environment, or to refer to polypeptides which have been expressed from a recombinant polynucleotide.

The method for the production of a polypeptide of the invention in recombinant form is itself included in the present invention, and is characterized in that the transformed cells, are cultured under conditions allowing the expression of a recombinant polypeptide encoded by a polynucleotide according to the invention, and in that the said recombinant polypeptide is recovered.

Also forming part of the invention is a method for the production of a heterologous polypeptide, characterized in that it uses a vector or a host cell according to the invention.

The recombinant polypeptides, characterized in that they are obtainable by the said method of production, also form part of the invention.

The recombinant polypeptides obtained as indicated above may be both in glycosylated and non-glycosylated form and may or may not have the natural tertiary structure.

These polypeptides may be produced from the polynucleotide, according to techniques for the production of recombinant polypeptides known to persons skilled in the art. In this case, the polynucleotide used is placed under the control of signals allowing its expression in a cellular host.

An effective system of production of a recombinant polypeptide requires having a vector and a host cell according to the invention.

These cells may be obtained by introducing into the host cells a nucleotide sequence inserted into a vector as defined above, and then culturing the said cells under conditions allowing the replication and/or expression of the transfected nucleotide sequence.

The methods for the purification of a recombinant polypeptide which are used are known to persons skilled in the art. The recombinant polypeptide may be purified from cell lysates and extracts, from the culture medium supernatant, by methods used individually or in combination, such as fractionation, chromatographic methods,

immunoaffinity techniques with the aid of specific mono- or polyclonal antibodies, and the like.

A preferred variant consists in producing a recombinant polypeptide fused with a "carrier" protein (chimeric protein). The advantage of this system is that it allows a stabilization and a reduction in proteolysis of the recombinant product, an increase in solubility during in vitro renaturation and/or simplification of the purification when the fusion partner has affinity for a specific ligand.

The invention also relates to the synthesis of synthetic polypeptides of the invention, in particular by chemical synthesis.

The polypeptides according to the present invention can be obtained by chemical synthesis using any of the numerous known peptide syntheses, for example the techniques using solid phases or techniques using partial solid phases, by condensation of fragments or by a conventional synthesis in solution.

Also forming part of the invention are the methods for the determination of the presence of a polynucleotide or a polypeptide encoded by involved in an protein-protein interaction of the present invention, characterized in that they use a polynucleotide or an antibody according to the invention.

These methods relate to, for example, the methods for the diagnosis *in vitro* of the presence in a biological sample of the procaryotic micro-organism from which said polypeptide is originating. The polynucleotide analysed may be either the genomic DNA, the cDNA or the mRNA.

These methods can use the probes and primers of the present invention.

The term "primer" denotes a specific oligonucleotide sequence which is complementary to a target nucleotide sequence and used to hybridize to the target nucleotide sequence. A primer serves as an initiation point for nucleotide polymerization catalyzed by either DNA polymerase, RNA polymerase or reverse transcriptase.

The term "probe" denotes a defined nucleic acid segment (or nucleotide analog segment, e.g., polynucleotide as defined hereinbelow) which can be used to identify a specific polynucleotide sequence present in samples, said nucleic acid segment comprising a nucleotide sequence complementary of the specific polynucleotide sequence to be identified.

They are generally purified nucleic sequences for hybridization comprising at least 12 nucleotides, preferably at least 15, 20 and 25 nucleotides, characterized in that they can hybridize specifically with the polynucleotide chosen encoding the polypeptide of interest involved in an protein-protein interaction of the present invention.

Among the methods for the determination of the presence of a polynucleotide encoding a polypeptide of interest involved in an protein-protein interaction of the present invention, the methods comprising at least one stage for the so-called PCR (polymerase chain reaction) or PCR-like amplification of the target polynucleotide according to the invention with the aid of a pair of primers of nucleotide sequences according to the invention are preferred.

PCR-like will be understood to mean all methods using direct or indirect reproductions of nucleic acid sequences, or alternatively in which the labelling systems have been amplified, these techniques are of course known, in general they involve the amplification of DNA by a polymerase; when the original sample is an RNA, it is advisable to carry out a reverse transcription beforehand. There are currently a great number of methods allowing this amplification, for example the so-called NASBA "Nucleic Acid Sequence Based Amplification" (Compton J. 1991 Nature. 350 (6313): 91-92), TAS "Transcription based Amplification System" (Guatelli et al., 1990, Proc. Natl. Acad. Sci. USA. 35: 273-286), LCR "Ligase Chain Reaction" (Landegren et al., 1998, Genome Research, 8:769-776), "Endo Run Amplification" (ERA), "Cycling Probe Reaction" (CPR), and SDA "Strand Displacement Amplification" (Walker et al., Nucleic Acids Res. 20: 1691-1696, 1992), methods well known to persons skilled in the art.

The invention comprises, in addition, methods for the determination of the presence of a polypeptide of interest involved in an protein-protein interaction of the present invention, characterized in that an antibody according to the invention is brought into contact with the biological material to be tested, under conditions allowing the possible formation of specific immunological complexes between the said polypeptide and the said antibody, and in that the immuno-logical complexes possibly formed are detected, such as, for example, methods using RIA or ELISA.

The transformed cells as described above can also be used as models so as to study the interactions between a polypeptide of the invention and their interacting

partners polypeptide, or between a polypeptide of the invention and chemical or protein compounds which are capable of modulating the protein-protein interaction according to the invention wherein said polypeptide of the invention is involved.

In particular, they may be used for the selection of products which interact with a polypeptide of the invention, or one of its SID® domains, as cofactor or as inhibitor, in particular a competitive inhibitor, or alternatively having an agonist or antagonist activity on the protein-protein interaction wherein said polypeptide of the invention is involved. Preferably, the said transformed cells will be used as a model allowing, in particular, the selection of products which make it possible to prevent and/or to treat pathologies induced by prokaryotic micro-organism.

Still another aspect of the invention pertains to a method for selecting an agent or compound capable of modulating the protein-protein interaction of a set of two polypeptides according to the invention comprising the steps of :

a) cultivating a recombinant cell clone containing a reporter gene expression of which is toxic for said recombinant cell clone and transformed with two plasmids wherein :

i) the first plasmid contains a nucleic construct comprising a nucleic sequence encoding a first hybrid polypeptide containing one of said two polypeptides and a DNA binding domain ;

ii) the second plasmid contains a nucleic construct comprising a nucleic sequence encoding a second hybrid polypeptide containing the second of said two polypeptides and an activating domain capable of activating said toxic reporter gene when the first and the second hybrid polypeptides are interacting ;

on a selective medium containing the agent to be tested and allowing the growth of said recombinant cell clone when the toxic reporter gene is not activated ; and

b) selecting agent which is capable of inhibiting the growth of the recombinant cell clone cultivated in step a).

The invention also comprises a method for selecting an agent or compound capable of modulating the protein-protein interaction of a set of two polypeptides according to the invention comprising the steps of :

a) cultivating a recombinant cell clone, preferably permeable, containing a reporter gene expression of which is toxic for said recombinant cell clone and transformed with two plasmids wherein :

i) the first plasmid contains a nucleic construct comprising a nucleic sequence encoding a first hybrid polypeptide containing one of said two polypeptides and the first domain of an enzyme ;

ii) the second plasmid contains a nucleic construct comprising a nucleic sequence encoding a second hybrid polypeptide containing the second of said two polypeptides and the second part of said enzyme capable of activating said toxic reporter gene when the first and the second hybrid polypeptides are interacting, said interaction restoring the activity of the enzyme ;

on a selective medium containing the agent to be tested and allowing the growth of said recombinant cell clone when the toxic reporter gene is not activated ; and

b) selecting agent which is capable of inhibiting the growth of the recombinant cell clone cultivated in step a).

In a preferred embodiment, said toxic reporter gene that can be used for negative selection, is URA3, CYH1 or CYH2 gene.

Still another aspect of the invention pertains to a method for selecting an agent or compound capable of modulating the protein-protein interaction of a set of two polypeptides according to the invention comprising the steps of :

a) cultivating a recombinant cell clone containing a reporter gene expression of which stimulates the growth of said recombinant cell clone and transformed with two plasmids wherein :

i) the first plasmid contains a nucleic construct comprising a nucleic sequence encoding a first hybrid polypeptide containing one of said two polypeptides and a DNA binding domain ;

ii) the second plasmid contains a nucleic construct comprising a nucleic sequence encoding a second hybrid polypeptide containing the second of said two polypeptides and an activating domain capable of activating said stimulating reporter gene when the first and the second hybrid polypeptides are interacting ;

on a selective medium containing the agent to be tested and allowing the normal growth of said recombinant cell clone when the stimulating reporter gene is not activated ; and

b) selecting agent which is capable of stimulating the growth of the recombinant cell clone cultivated in step a).

In a preferred embodiment, the method according to the invention for selecting an agent or compound capable of modulating the protein-protein interaction of a set of two polypeptides is a method for selecting an agent capable of modulating the interaction between a polypeptide encoded by the ORF HP1198 (or a fragment thereof, preferably one of its SID® domains, or homologuous polypeptide thereof exhibiting at least 80 % identity degree) and a polypeptide encoded by the ORF HP1293 (or a fragment thereof, preferably one of its SID® domains, or homologuous polypeptide thereof exhibiting at least 80 % identity degree).

In a preferred embodiment, the method according to the invention for selecting an agent or compound capable of modulating the protein-protein interaction of a set of two polypeptides is a method for selecting an agent capable of modulating the interaction between a polypeptide encoded by the ORF HP1198 (or a fragment thereof, preferably one of its SID® domains, or homologuous polypeptide thereof exhibiting at least 80 % identity degree) and a polypeptide encoded by the ORF HP0088 (or a fragment thereof, preferably one of its SID® domains, or homologuous polypeptide thereof exhibiting at least 80 % identity degree).

In a preferred embodiment, the method according to the invention for selecting an agent or compound capable of modulating the protein-protein interaction of a set of two polypeptides is a method for selecting an agent capable of modulating the interaction between a polypeptide encoded by the ORF HP1198 (or a fragment thereof, preferably one of its SID® domains, or homologuous polypeptide thereof exhibiting at least 80 % identity degree) and a polypeptide encoded by the ORF HP1032 (or a fragment thereof, preferably one of its SID® domains, or homologuous polypeptide thereof exhibiting at least 80 % identity degree).

In another embodiment of the invention, inventors provide a kit for screening a modulator agent comprising at least one recombinant diploid clone or a cell clone, haploid or diploid, transformed with a plasmid containing a sequence coding for a bait polypeptide and a plasmid containing the nucleotide sequence of a SID® or of homologue polypeptide of SID®, said plasmids may be chosen between pACTIIst and pAS2ΔΔ.

SID® or homologue sequence of SID® acting on the same pair of interacting proteins may be also modulator agents.

Modulator agent selected by anyone of the yeast or bacterial two-hybrid system method of the invention also forms part of the invention.

These modulator agents of protein-protein interaction according to the invention may be obtained for example from a library of compounds.

Consequently, is also part of the invention a modulator agent selected by the method of the invention previously described capable of interfering with a protein-protein interaction according to the invention. This agent may modulate an interaction of the invention between two prokaryotic polypeptides, particularly between two *Helicobacter pylori*, *Escherichia coli*, *Staphylococcus aureus* or *Streptococcus pneumoniae* polypeptides, or between a prokaryotic polypeptide, such as *Helicobacter pylori*, *Staphylococcus aureus* or *Streptococcus pneumoniae* polypeptide, and a polypeptide originating from a host organism of said prokaryotic micro-organism, such as mammal, particularly human.

These methods allow the selection of chemical or biochemical compound capable of interacting, directly or indirectly, with the polynucleotide or the polypeptide encoded by of the invention, in particular capable of modulating the protein-protein interaction wherein said polypeptide of the invention is involved.

More particularly, the invention concerns modulator agent capable of modulating, more preferred of inhibiting, the viability and/or the growth of the prokaryotic micro-organism, preferrably *Helicobacter pylori*, *Staphylococcus aureus* or *Streptococcus pneumoniae*, from which is the protein-protein interaction.

For the screening of compounds capable of modulating the protein-protein interaction wherein said polypeptide of the invention is involved, the preferred principal effect is the effect of inhibiting the viability and/or the growth of the prokaryotic micro-organism, preferrably *Helicobacter pylori*, *Staphylococcus aureus* or *Streptococcus pneumoniae*, from which is the protein-protein interaction.

These effects of modulating the viability and/or the growth of prokaryotic micro-organisms can be analysed by any method known by a skilled man.

For example, a screening method of modulating agent can comprise the following steps :

- Select one specific interaction.

- Transform a permeabilized yeast cell with plasmids containing bait polypeptide and prey polypeptide of the specific interaction.

- Plate a top agar containing transformed permeabilized yeast cells on square boxes (that already contains agarose gel).

- Apply by spotting the compounds to test on top agar as soon as it is solidified.

- Incubate, for example overnight at 30°C, and

- Analyse results : select lead compounds that prevent transformed permeabilized yeast cells from growing.

Screening may be used to test compounds capable of modifying the level and/or the specificity of expression of the polynucleotide or the polypeptide encoded by of the invention involved in the protein-protein interaction according to the invention.

A quantitative or qualitative analysis of the expression of the gene encoded the polypeptide of the invention involved in the protein-protein interaction according to the invention can be carried out using primers or probes of the invention as DNA templates, the term DNA templates designating nucleic acids having a sufficient length to allow a specific detection of the expression of mRNAs capable of hybridizing thereto. For example, the DNA templates contain nucleic acids derived from said gene, or sequences complementary thereto for which it is desired to estimate the level or the specificity of expression, and comprising at least 15, at least 25, at least 50, at least 100 or at least 500 consecutive nucleotides.

Another aspect of the present invention consists in methods of identifying molecules capable of binding to one of the set of two polypeptides of the invention involved in the protein-protein interaction. Such molecules can be used to modulate the viability and/or the growth of the prokaryotic micro-organism, preferrably *Helicobacter pylori*, from which is the protein-protein interaction activity. For example, such molecules can be used to stimulate or to inhibit a biological reaction involved in the viability and/or the growth of the prokaryotic micro-organism.

Numerous methods well known by the skilled man exist for identifying ligands for a defined polypeptide.

For example to identifying molecules capable of binding to one polypeptide of the set of two polypeptides of the invention involved in the protein-protein interaction, a subunit thereof or a fragment thereof comprising at least 10, at least 20, at least 30, or

more than 30 consecutive amino acids with small molecules such as those generated by combinatory chemistry, it is possible to use an HPLC-coupled microdialysis, or an affinity capillary electrophoresis.

In other methods, the peptides or small molecules capable of interacting with said one of the set of two polypeptides of the invention, a subunit thereof or a fragment thereof may be linked to detectable markers such as radioactive, fluorescent or enzymatic markers. These labelled molecules are brought into contact with the immobilized said one of the set of two polypeptides of the invention, under conditions allowing a specific interaction. After elimination of the molecules which are not specifically bound, the bound molecules are detected by appropriate means.

In addition, the peptides or small molecules which bind to said one of the set of two polypeptides of the invention, preferably to its SID® binding site can be identified by competition experiments. In such experiments, said one of the set of two polypeptides of the invention, is immobilized on a surface. Increasing quantities of peptides or of small molecules are brought into contact with the immobilized said one of the set of two polypeptides of the invention in the presence of the second labelled polypeptide of said two polypeptides of the invention, designated labelled ligand. The labelled ligand may be labelled with a radioactive, fluorescent or enzymatic marker. The capacity of the molecule tested to interact with said one of the set of two polypeptides of the invention is determined by measuring the quantity of labelled ligand bound in the presence of the molecule tested. A decrease in the quantity of bound ligand when the molecule tested is present indicates that the latter is capable of interacting with said one of the set of two polypeptides of the invention.

The Biacore™ technology can also be used to carry out the screening of compounds capable of interacting with said one of the set of two polypeptides of the invention. This technology is described in Szabo et al. (1995) and in Edwards and Leartherbarrow (Analytical Biochemistry, 246, 1-6, 1997), of which the teaching is incorporated by reference, and makes it possible to detect interactions between molecules in real time without the use of labelling.

One of the main advantages of this method is that it allows the determination of the association constants between said one of the set of two polypeptides of the

invention and the interacting molecules. Thus, it is possible to specifically select the molecules interacting with high or low association constants.

The proteins or other molecules interacting said one of the set of two polypeptides of the invention can be identified using affinity columns which contain said one of the set of two polypeptides of the invention. Said one of the set of two polypeptides of the invention may be attached to the column using conventional techniques including chemical coupling to an appropriate column matrix such as agarose, Affi Gel, or other matrices known to a person skilled in the art. In another aspect of the invention, the affinity column may contain chimeric proteins in which said one of the set of two polypeptides of the invention would be fused, for example, with glutathione S-transferase. The molecules to be tested which are described above are then deposited on the column. The molecules interacting said one of the set of two polypeptides of the invention are retained by the column and can be isolated by elution.

The chemical or biochemical compounds, characterized in that they make it possible to modulate, directly or indirectly, the protein-protein interaction according to the invention, and selected by the said methods defined above, also form part of the invention.

The use of a polypeptide according to the invention for the modulation of *Helicobacter pylori*'s protein interaction, also forms part of the present invention.

Still another aspect, the present invention is directed to a method for the production of monoclonal or polyclonal antibodies comprising the step of immunization of an animal or human organism with an immunogenic agent comprising a polypeptide, a vector according or a host cell according to the invention, and to antibodies obtained by said method.

The mono- or polyclonal antibodies or fragments thereof, chimeric or immuno-conjugated antibodies, characterized in that they are capable of specifically recognizing a polypeptide according to the invention, also form part of the invention.

As used herein, the term "antibody" refers to a polypeptide or group of polypeptides which are comprised of at least one binding domain, where an antibody binding domain is formed from the folding of variable domains of an antibody molecule to form three-dimensional binding spaces with an internal surface shape and charge distribution complementary to the features of an antigenic determinant of an antigen,

which allows an immunological reaction with the antigen. Antibodies include recombinant proteins comprising the binding domains, as wells as fragments, including Fab, Fab', F(ab)2, and F(ab')2 fragments.

Specific polyclonal antibodies may be obtained from a serum of an animal immunized against a polypeptide according to the invention, in particular produced by genetic recombination or by peptide synthesis, according to the customary procedures, from a polynucleotide according to the invention.

The specific monoclonal antibodies may be obtained according to the conventional hybridoma culture method described by Kohler and Milstein (Kohler, G. and Milstein, C., Nature 256:495, 1975).

The antibodies according to the invention are, for example, chimeric antibodies, humanized antibodies, Fab or F(ab')2 fragments. They may also be in the form of immunoconjugates or of labelled antibodies so as to obtain a detectable and/or quantifiable signal (Harlow, E., and D. Lane. 1988. Antibodies A Laboratory Manual. Cold Spring Harbor Laboratory. pp. 53-242).

The invention also relates to methods for the detection and/or purification of a polypeptide according to the invention, characterized in that they use an antibody according to the invention.

The invention comprises, in addition, purified polypeptides, characterized in that they are obtained by a method according to the invention.

Moreover, in addition to their use for the purification of polypeptides, the antibodies of the invention, in particular the monoclonal antibodies, may also be used for the detection of these polypeptides in a biological sample.

They thus constitute a means for the immunocytochemical or immuno-histochemical analysis of the expression of polypeptide against which they are raised on specific tissue sections, for example by immunofluorescence, gold labelling, enzymatic immunoconjugates.

They make it possible in particular to detect expression of these polypeptides in the biological tissues or samples, which makes them useful for monitoring the progress of a method of prevention or treatment.

More generally, the antibodies of the invention may be advantageously used in any situation where the expression of a polypeptide of the invention against which they are raised needs to be observed.

The invention finally relates to a polynucleotide, a polypeptide, a vector, a host cell, a modulator agent or an antibody to the invention as compound for the preparation of a medicament.

So the invention also encompasses a pharmaceutical composition comprising a compound selected from the group consisting of :

a) a polynucleotide according to the invention ;

b) a polypeptide according to the invention ;

c) a vector according to the invention ;

d) a host cell according to the invention ;

e) a modulator agent to the invention ; and

f) an antibody to the invention.

A pharmaceutical composition according to the invention, wherein said composition is administered by any route such as intravenous route, intramuscular route, oral route, or mucosal route with an acceptable physiological carrier and/or adjuvant, also forms part of the invention.

The compounds according to the invention as a medicament for the prevention and/or treatment of pathologies of infection diseases induced by prokaryotic micro-organism are particularly preferred.

The most preferred are the compounds according to the invention, as a medicament for the prevention and/or treatment of infection diseases induced by *Helicobacter pylori, Staphylococcus aureus* or *Streptococcus pneumoniae*.

The compounds of the invention as active ingredients of a medicament will be preferably in soluble form, combined with a pharmaceutically acceptable vehicle.

Such compounds which can be used as a medicament offer a new approach for preventing and/or treating pathologies linked to infection by prokaryotic micro-organism such as *Helicobacter pylori, Staphylococcus aureus* or *Streptococcus pneumoniae*. Preferably, these compounds will be administered by the systemic route, in particular by the intravenous route, by the intramuscular or intradermal route or by the oral route.

Their modes of administration, optimum dosages and galenic forms can be determined according to the criteria generally taken into account in establishing a treatment suited to a patient, such as for example the age or body weight of the patient, the seriousness of his general condition, the tolerance to treatment and the side effects observed, and the like.

The identified compounds can be administered to a mammal, including a human patient, alone or in pharmaceutical compositions where they are mixed with suitable carriers or excipient(s) at therapeutically effective doses to treat disorders associated with prokaryotic micro-organism infection. Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences", Mack Publishing Co., Easton, PA, latest edition.

Suitable routes of administration include oral, rectal, transmucosal, or intestinal administration, parenteral delivery, including intramuscular, subcutaneous, injections, as well as intravenous, intraperitoneal or intranasal injections.

Pharmaceutical compositions and medicaments for use in accordance with the present invention may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries. Proper formulation is dependent upon the route of administration chosen.

For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer such as a phosphate or bicarbonate buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with fillers such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All

formulations for oral administration should be in dosages suitable for such administration.

For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebulizer, with the use of a suitable gaseous propellant, e.g., carbon dioxide. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, e.g., gelatin, for use in an inhaler or insufflator, may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch.

The compounds may be formulated for parenteral administration by injection, e.g., by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, e.g., in ampoules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Aqueous suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions.

Alternatively, the active ingredient may be in powder or lyophilized form for constitution with a suitable vehicle, such as sterile pyrogen-free water, before use.

Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days.

Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols.

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve their intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amounts is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein.

For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes or encompasses a concentration point or range shown the desired effect in an in vitro system. Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD50, (the dose lethal to 50 % of the test population) and the ED50 (the dose therapeutically effective in 50 % of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD5O and ED5O. Compounds which exhibit high therapeutic indices are preferred.

The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED50, with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the

patient's condition (see, e.g., Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1).

Dosage amount and interval may be adjusted individually to provide plasma levels of the active compound which are sufficient to maintain the modulating effects. Dosages necessary to achieve the modulating effect will depend on individual characteristics and route of administration.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

Other characteristics and advantages of the invention appear in the remainder of the description with the examples and figures whose legends are represented below.

Examples

Medium composition and standard protocols are available in Sambrook and Maniatis (Sambrook, J., Fritsch, E.F., and T. Maniatis. (1989) Molecular Cloning: A Laboratory Manual. 2ed. Cold Spring Harbor Laboratory, Cold Spring Harbor, New York).

Example 1 : Preparation of a *Helicobacter pylori* genomic collection

1.A. Collection preparation and transformation in *Escherichia coli*

1.A.1. Fragmented of genomic DNA preparation

The *Helicobacter pylori* genomic DNA is fragmented in a nebulizer (GATC) for 1 minute, precipitated and resuspended in water.

The obtained nebulized genomic DNA is successively treated with Mung Bean Nuclease (Biolabs) (30 minutes at 30°C), T4 DNA polymerase (Biolabs) (10 minutes at 37°C) and Klenow enzyme (Pharmacia) (10 minutes at room temperature and 1 hour at 16°C).

DNA is then extracted, precipitated and resuspended in water.

1.A.2. Ligation of linkers to blunt-ended genomic DNA

Oligonucleotide PL160 (5' end phosphorylated) 1 µg/µl and PL159 2µg/µl.

Sequence of the oligo PL160 : 5'-ATCCCGGACGAAGGCC-3'.

Sequence of the oligo PL159 : 5'-GGCCTTCGTCCGG-3'.

Linkers were preincubated (5 minutes at 95°C, 10 minutes at 68°C, 15 minutes at 42°C) then cooled down at room temperature and ligated with genomic DNA inserts at 4°C overnight.

Linkers were further removed on a separation column (Chromaspin TE 400, Clontech), according to the manufacturer protocol.

1.A.3. Vector preparation

pACTIIst is successively digest with BamHI restriction enzyme (Biolabs) for 1 hour at 37°C, dephosphorylated with Calf Intestine Phosphatase (CIP) (Biolabs) and filled in with dGTP using Vent DNA polymerase (exo-) (Biolabs), extracted, precipitated and resuspended in water.

1.A.4. Ligation between vector and insert of genomic DNA

The prepared vector is ligated overnight at 15°C with the genomic blunt ended DNA described in section 2 using T4 DNA ligase (Biolabs). The DNA is then precipitated and resuspended in water.

1.A.5. Library transformation in *Escherichia coli*

Transform DNA from section 1.A.4 into Electromax DH10B electrocompetent cells (Gibco BRL) with Cell Porator apparatus (Gibco BRL). Add 1 ml SOC medium and incubate transformed cells at 37°C for 1 hour. Add 9 ml volume of SOC medium per tube and plate on LB+ampicillin medium. Scrape colonies with liquid LB medium. Aliquot and freeze at -80°C.

The obtained collection of recombinant cell clones is named HGXBHP1 (CNCM No I-2181 deposited on April 13, 1999).

1.B. Collection transformation in *Saccharomyces cerevisiae*

The *Saccharamyces cerevisiae* strain (Y187 (MATα Gal4Δ Gal80Δ ade2-101 His3 Leu2-3, -112 Trp1-901 Ura3-52 URA3::UASGAL1-LacZ Met)) transformed with the HGXBHP1 *H. pylori* genomic DNA library.

The plasmid DNA contained in *E. coli* are extracted (Qiagen) from aliquoted *E. coli* frozen cells (1.A.5.).

Grow *Saccharomyces cerevisiae* yeast Y187 in YPGlu.

Yeast transformation is performed according to standard protocol (Giest *et al.* Yeast, 11, 355-360, 1995) using yeast carrier DNA (Clontech). This experiment leads to

10^4 to 5.10^4 cells/µg DNA. Spread an estimating of 2.10^4 transformanton DO-Leu (Drop-out) medium per plates. Aliquot and freeze at -80°C.

1.C. Construction of bait plasmid

The genomic amplification of the ORF is obtained by PCR using the Pfu proofreading Taq polymerase (Stratagene) and 200 ng of genomic DNA as template. PCR primers are chosen in regions flanking the ORF.

Set up the PCR program as followed :

94°	45''	
94°	45''	
48°	45''	x 30 cycles
72°	6'	
72°	10'	
15°	∞	

Check amplification on agarose gel.

Purify PCR fragments with Qiaquick column (Qiagen) according to the manufacturer protocol.

Digest purified PCR fragments with adequate restriction enzymes.

Purify PCR fragments with Qiaquick column (Qiagen) according to the manufacturer protocol.

Ligate digested PCR fragments into an adequately digested and dephosphorylated bait vector (pAS2ΔΔ) according to standard protocol (Maniatis *et al.*).

Transform into competent bacterial cells. Grow cells, extract DNA and sequence plasmid.

This protocole may also be applied to *E. coli*, *S. aureus* and *S. pneumoniae* genomic DNA.

Example 2 : Screening the collection with the two-hybrid in yeast system

2.A. The mating protocol

We have chosen the mating two-hybrid in yeast system (firstly described by Fromont Racine et al., Nature Genetics, 1997, vol. 16, 277-282, Toward a functional analysis of the yeast genome through exhaustive two-hybrid screens) for its advantages but we could also screen the *Helicobacter pylori* collection in classical two-hybrid system as described in Fields *et al.* or in a yeast reverse two-hybrid system.

The mating procedure allows a direct selection on selective plates because the two fusion proteins are already produced in the parental cells. No replica plating is required.

This protocol is written for the use of the library transformed into the Y187 strain.

Before mating, transform *S. cerevisiae* (CG 1945 strain (MATa Gal4-542 Gal180-538 ade2-101 His3*200 Leu2-3,-112 Trp1-901 Ura3-52 Lys2-801 URA3::GAL4 17mers (X3)-CyC1TATA-LacZ LYS2::GAL1UAS-GAL1TATA-HIS3 CYH^R)) according to step 1.B. and spread on DO-Trp medium.

Day 1, morning : preculture

Preculture of Y187 cells carrying the bait plasmid obtained at step 1.C. in 20 ml DO-Trp medium. Grow at 30°C with vigorous agitation.

Day 1, late afternoon : culture

Measure OD_{600nm} of the DO-Trp preculture of Y187 cells carrying the bait plasmid preculture.

Inoculate 150 ml DO-Trp at OD600nm 0.006/ml, grow overnight at 30°C with vigorous agitation.

Day 2 : mating

medium and plates

5 YPGlu plates (Rich medium with glucose)

50 ml tube with 30 ml DO-Leu-Trp-His

100 ml flask with 20 ml of YPGlu

75 DO-Leu-Trp-His plates

2 DO-Leu plates

2 DO-Trp plates

2 DO-Leu-Trp plates

Measure OD600nm of the DO-Trp culture. It should be around 1.

For the mating, you must use twice as many bait cells as library cells. To get a good mating efficiency, you must collect the cells at 10^8 cells per cm^2.

Estimate the amount of bait culture (in ml) that makes up 80 OD600nm units for the mating with the prokaryote library.

Thaw a vial containing the HGXYHP1 library slowly on ice. Add the contents of the vial to 20 ml YPGlu. Let those cells recover at 30°C, under gentle agitation for 10 minutes.

Mating

Put the 80 OD_{600nm} units of bait culture into a 250 ml flask.

Add the HGXYHP1 library culture to the bait culture. Transfer the mixture of diploids into 50 ml sterile tubes. Centrifuge, discard the supernatant and resuspend in YPGlu medium.

Distribute cells on YPGlu Plates (Rich medium with glucose).

Incubate plates cells-up at 30°C for 4h30min.

Collection of mated cells

Wash and rinse plates and spread collected cells on DO-Leu-Trp-His plates.

Day 4

Selection of clones capable of growing on DO-Leu-Trp-His : this medium allows us to isolate diploid clones presenting an interaction.

Count the His+ colonies on control plates.

The number of His+ cell clones will define which protocol is to be processed :

Upon 20.10^6 His+ colonies :

- if number of His+ cell clones > 285 : then process overlay and then luminometry protocols on blue colonies (2.B and 2.C) ;
- if number of His+ cell clones < 285 : process luminometry protocol (2.C).

The following step leads to the selection of the strongest interaction.

2.B. The X-Gal overlay assay

X-Gal overlay assay is performed directly on the selective medium plates after scoring the number of His^+ colonies.

Material

Set up a waterbath. The water temperature should be 50°C.

- 0.5 M Na_2HPO_4 pH 7.5.
- 1.2 % Bacto-agar.
- 2 % X-Gal in DMF (dimethyl formamide).

- Overlay mixture : 0.25 M Na_2HPO_4 pH7.5, 0.5 % agar, 0.1 % SDS (Sodium dodecyl sulfate), 7 % DMF (LABOSI), 0.04 % X-Gal (ICN). For each plate, 10 ml overlay mixture are needed.
- DO-leu-trp-his plates.
- Sterile toothpicks.

Experiment

Temperature of the overlay mix should be between 45 and 50°C.

Pour the overlay-mix over the plates in portions of 10 ml.

Collect them when the top layer is settled.

Incubate plates overlay-up at 30°C. Note the time.

Check for blue colonies regularly. If no blue colony appears, wait for overnight incubation. Mark with a pen and number the positives.

Streak the positives colonies on fresh DO-Leu-Trp-His plates with a sterile toothpick.

2.C. The luminometry assay

Grow His+ colonies overnight at 30°C in microtiter plates containing DO-Leu-Trp-His+Tetracyclin medium with shaking. The day after, dilute 15 times overnight culture into a new microtiter plate containing the same medium. Incubate 5 hours at 30°C with shaking. Dilute samples 5 times and read OD_{600nm}. Dilute again to obtain between 10 000 and 75 000 yeast cells/well in 100 µl final volume.

Per well, add 76 µl of One Step Yeast Lysis Buffer (Tropix), 20 µl SapphireII Enhancer (Tropix), 4 µl Galacton Star (Tropix), incubate 40 minutes at 30°C.

Measure the β-Gal read-out (L) using a Luminometer (Trilux, Wallach).

Calculate value of OD_{600nm}/L and select interacting preys having highest values.

At this step of the protocol, we have isolated diploid cell clones presenting interaction. The next step is now to identify polypeptides involved in the selected interactions.

Example 3 : Identification of positive clones

3.A. PCR on yeast colonies

Introduction

PCR amplification of fragments of plasmid DNA directly on yeast colonies is a quick and efficient procedure to identify sequences cloned into this plasmid. It is directly derived from a published protocol (Wang H. et al., Analytical Biochemestry, 237, 145-146, 1996). However, it is not a standardized protocol : in our hands it varies from strain to strain, it is dependent of experimental conditions (number of cells, Taq polymerase source, etc). This protocol should be optimized to specific local conditions.

Materials

- For 1 well, PCR mix composition is :

32.5 µl water,

5 µl 10X PCR buffer (Pharmacia),

1 µl dNTP (10 mM each)

0.5 µl Taq polymerase (5u/µl) (Pharmacia),

0.5 µl oligonucleotide ABS1 10 pmole/µl: 5'-GCGTTTGGAATCACTACAGG-3',

0.5 µl oligonucleotide ABS2 10 pmole/µl: 5'-CACGATGCACGTTGAAGTG-3'.

- 1 N NaOH.

Experiment

Grow positive colonies overnight at 30°C on a 96 well cell culture cluster (Costar), containing 150 µl DO-Leu-Trp-His+Tetracyclin with shaking. Resuspend culture and transfer immediately 100 µl on a Thermowell 96 (Costar).

Centrifuge 5 minutes at 4000 rpm at room temperature.

Remove supernatant.

Place the Thermowell in the thermocycler (GeneAmp 9700, Perkin Elmer) 5 minutes at 99.9°C and then 10 minutes at 4°C.

Add lysis buffer and incubate.

Centrifuge, transfer aliquot of supernatant in each well, add PCR mix, shake well.

Set up the PCR program as followed :

94°C	3 minutes	
94°C	30 secondes	x 35 cycles
53°C	1 minute 30 secondes	
72°C	3 minutes	

72°C 5 minutes

15°C ∞

Check the quality, the quantity and the length of the PCR fragment on agarose gel.

The length of the cloned fragment is the estimated length of the PCR fragment minus 300 base pairs that correspond to the amplified flanking plasmid sequences.

3.B. Plasmids rescue from yeast by electroporation

Introduction

The previous protocol of PCR on yeast cell may not be successful, in such a case, we rescue plasmids from yeast by electroporation. This experiment allows the recovery of prey plasmids from yeast cells by transformation of *E. coli* with a yeast cellular extract. We can then amplify the prey plasmid and sequence the cloned fragment.

Material

Plasmid rescue

Glass beads 425-600 µm (Sigma)

Phenol/chloroform (1/1) premixed with isoamyl alcohol (Amresco)

Extraction buffer : 2 % Triton X100, 1 % SDS, 100 mM NaCl, 10 mM TrisHCl pH 8.0, 1 mM EDTA pH 8.0.

Mix ethanol/NH_4Ac : 6 volumes ethanol with 7.5 M NH_4 Acetate, 70 % Ethanol and yeast cells in patches on plates.

Electroporation

SOC medium

M9 medium

Selective plates : M9-Leu+Ampicillin

2 mm electroporation cuvettes (Eurogentech)

Experiment

Plasmid rescue

Prepare cell patch on DO-Leu-Trp-His with cell culture of section 2.C.

Scrape the cell of each patch in Eppendorf tube, add 300 µl of glass beads in each tube, then, add 200 µl extraction buffer and add 200 µl phenol:chloroform:isoamyl alcohol (25:24:1).

Centrifuge tubes 10 minutes at 15000 rpm.

Transfer 180 µl supernatant to a sterile Eppendorf tube and add to each 500 µl ethanol/NH_4Ac, vortex.

Centrifuge tubes 15 minutes, 15000 rpm at 4°C.

Wash pellet with 200 µl 70 % ethanol, remove ethanol and dry pellet.

Resuspend pellet in 10 µl water. Store extracts at -20°C.

Electroporation

Material : Electrocompetent MC1066 cells prepared according to standard protocols (Maniatis).

Add 1 µl of yeast plasmid DNA-extract to pre-chilled Eppendorf tube, and keep on ice.

Mix 1 µl plasmid yeast DNA-extract sample, add 20 µl electrocompetent cells and transfer in a cold electroporation cuvette.

Set the Biorad electroporator on 200 ohms resistance, 25 µF capacity ; 2.5 kVolts.

Place cuvette in the cuvette holder and electroporate.

Add 1 ml SOC into the cuvette and transfer the cell-mix into sterile Eppendorf tube.

Let cells recover for 30 minutes at 37°C, spin the cells down 1 minute, 4000x g and pour off supernatant. Keep about 100 µl medium and use it to resuspend the cells and spread them on selective plates (e.g. M9-Leu plates).

Incubate plates for 36 hours at 37°C.

Grow one colony and extract plasmids. Check presence and size of insert through enzymatic digestion and agarose gel. Sequence insert.

Example 4 : Protein-Protein Interactions

For the purpose of this example, we have chosen to study *Helicobacter pylori*'s protein-protein interactions.

For each bait, the previous protocol leads to the identification of prey polynucleotide sequences. In order to identify a protein-protein interaction, we need to characterize the obtained prey polypeptide sequence regarding the *Helicobacter pylori* genome.

This may be accomplish with a software program names blastwun (available on the Internet site of the University of Washington : http://bioweb.pasteur.fr/seqanal/interfaces/blastwu.html, this is a development version of software for gene and protein identification through similarity searches of protein and nucleotide sequence databases).

Blastwun program compares prey polypeptide insert sequence (rescued from prey plasmid) with whole *Helicobacter pylori* genome (available on N.C.B.I. web site : http://www.ncbi.nlm.nih.gov under GenBank accession number AE000511). This comparison leads to prey polynucleotide localizations in *H. pylori* genome, each localization having a score depending on the homology of sequence. For each prey polynucleotide, we consider the localization with the highest score and, if the insert sequence is included in and is in phase with an Open Reading Frame, we can identify one prey polypeptide interacting with one bait polypeptide.

Helicobacter pylori ORF's sequences are available on the World-Wide Web site of The Institute for Genomic Research (TIGR) at http://www.tigr.org/tdb/mbd/hpdb/hpdb.html.

This web page allows several request concerning *Helicobacter pylori's* genome, in particular, its ORF sequence. To get the sequences of a specific ORF, click on the window named « HP# » and click search. This operation leads to a new web page presenting nucleic and peptide sequence of the specific ORF.

Table I : protein interaction in *Helicobacter pylori* (see hereafter)

Example 5 : Identification of SID®

Experiment results in step 4. sequences of each prey fragment encoding for an interacting prey polypeptide.

By comparing and selecting the intersection of every isolated fragments that are included in the same polypeptide, we define the Selected Interacting Domain (SID®) see figure 7.

See results in Tables II and III.

Table I : Interaction involving polypeptides including *Helicobacter pylori* ORF

Bait polypeptides (ORF reference according to Tomb et al.)	Interacting ORF (ORF reference according to Tomb et al.)
HP0047	HP0047
HP0047	HP0048
HP0047	HP0695
HP0061	HP0066
HP0061	HP0978
HP0061	HP1409
HP0064	HP0063
HP0066	HP0066
HP0067	HP0069
HP0067	HP0609
HP0067	HP0768
HP0067	HP0770
HP0067	HP0956
HP0068	HP0070
HP0068	HP0118
HP0069	HP0067
HP0070	HP0068
HP0070	HP0070
HP0071	HP0278
HP0071	HP0417
HP0071	HP0570
HP0071	HP0775
HP0071	HP1340
HP0071	HP1409
HP0072	HP1489
HP0073	HP0073
HP0073	HP0232

HP0073	HP0259
HP0073	HP0067
HP0073	HP0232
HP0073	HP0705
HP0268	HP1198
HP0289	HP0289
HP0289	HP0289
HP0289	HP0887
HP0289	HP0922
HP0289	HP1038
HP0289	HP1543
HP0289	HP0289
HP0289	HP0289
HP0289	HP0610
HP0289	HP1355
HP0311	HP0312
HP0338	HP0132
HP0338	HP0337
HP0391	HP0099
HP0391	HP0392
HP0691	HP0692
HP0691	HP1362
HP0697	HP0012
HP0697	HP0048
HP0697	HP0558
HP0697	HP0599
HP0697	HP0696
HP0697	HP0864
HP0697	HP1037
HP0697	HP1038
HP0697	HP1299

HP0697	HP1576
HP0776	HP0067
HP0776	HP0278
HP0776	HP1378
HP0776	HP1409
HP0797	HP0289
HP0797	HP0887
HP0797	HP1349
HP0797	HP1377
HP0797	HP1409
HP0800	HP0433
HP0800	HP0687
HP0800	HP0800
HP0800	HP0801
HP0800	HP0924
HP0800	HP1267
HP0800	HP1460
HP0801	HP0152
HP0801	HP0800
HP0801	HP1513
HP0868	HP0088
HP0868	HP0327
HP0868	HP0869
HP0868	HP1142
HP0874	HP0875
HP0875	HP0874
HP0887	HP0459
HP0887	HP0610
HP0887	HP0699
HP0887	HP0887
HP0887	HP1157

HP0887	HP1460
HP0887	HP1464
HP0887	HP0610
HP0887	HP0887
HP0887	HP1157
HP0887	HP1464
HP0935	HP0072
HP0935	HP0528
HP0935	HP0657
HP0978	HP0979
HP0978	HP1583
HP1032	HP0643
HP1032	HP0818
HP1032	HP1122
HP1032	HP1198
HP1032	HP1316
HP1067	HP0392
HP1198	HP0088
HP1198	HP0268
HP1198	HP0293
HP1198	HP0452
HP1198	HP0705
HP1198	HP0775
HP1198	HP0965
HP1198	HP1032
HP1198	HP1114
HP1198	HP1124
HP1198	HP1198
HP1198	HP1274
HP1198	HP1378
HP1198	HP1411

HP1198	HP1541
HP1198	HP1032
HP1198	HP1218
HP1230	HP1230
HP1230	HP1529
HP1231	HP1247
HP1244	HP0857
HP1244	HP1246
HP1246	HP0121
HP1246	HP0326
HP1246	HP0407
HP1246	HP0886
HP1246	HP1035
HP1246	HP1244
HP1246	HP1460
HP1247	HP1231
HP1247	HP1353
HP1293	HP1198

* Tomb et al., 1997, Nature, 388, 539-547

As indicated page 547 in the document Tomb et al., the annotated *H. pylori* genome sequence and gene family alignments are avalaible on the World-Wide Web site at http://www.tigr.org/tdb/mbd/hpdb/hpdb.html. For each ORF referenced HPXXXX, the detailed nucleic sequence, and amino acids sequence encoded by, can be obtained on the World-Wide Web site at http://www.tigr.org/tdb/mbd/hpdb/hpdb.html. by introducing said reference HPXXXX (see example 4).

Table II :

Bait polypeptides (ORF reference according to Tomb et al.)	SID® Amino Acid Sequence (SEQ ID N°)
HP0868	2
HP0868	4
HP0868	6
HP0868	8
HP0800	10
HP0800	12
HP0800	14
HP0800	16
HP0800	18
HP0800	20
HP0800	22
HP0801	24
HP0801	26
HP0801	28
HP0887	30
HP0887	32
HP0887	34
HP0887	36
HP0887	38
HP0887	40
HP0887	42
HP0289	44
HP0289	46
HP0289	48
HP0289	50
HP0289	52
HP0289	54

HP0289	56
HP0289	58
HP0289	60
HP0289	62
HP0068	64
HP0068	66
HP0047	68
HP0047	70
HP0047	72
HP0069	74
HP0066	76
HP0268	78
HP1293	80
HP0061	82
HP0061	84
HP0061	86
HP0064	88
HP1198	90
HP1198	92
HP1198	94
HP1198	96
HP1198	98
HP1198	100
HP1198	102
HP1198	104
HP1198	106
HP1198	108
HP1198	110
HP1198	112
HP1198	114
HP1198	116

HP1198	118
HP1231	120
HP1032	122
HP1032	124
HP1032	126
HP1032	128
HP1032	130
HP1230	132
HP1230	134
HP1529	136
HP0978	138
HP0978	140
HP0071	142
HP0071	144
HP0071	146
HP0071	148
HP0071	150
HP0071	152
HP0073	154
HP0073	156
HP0073	158
HP0935	160
HP0935	162
HP0935	164
HP0338	166
HP0338	168
HP1246	170
HP1246	172
HP1246	174
HP1246	176
HP1246	178

HP1246	180
HP1246	182
HP0797	184
HP0797	186
HP0797	188
HP0797	190
HP0797	192
HP0311	194
HP0067	196
HP0067	198
HP0067	200
HP0067	202
HP0067	204
HP1244	206
HP1244	208
HP1067	210
HP0875	212
HP0776	214
HP0776	216
HP0776	218
HP0776	220
HP0697	222
HP0697	224
HP0697	226
HP0697	228
HP0697	230
HP0697	232
HP0697	234
HP0697	236
HP0697	238
HP0697	240

HP0887	242
HP0887	244
HP0887	246
HP0887	248
HP1247	250
HP1247	252
HP0874	254
HP0072	256
HP0391	258
HP0391	260
HP0070	262
HP0070	264
HP0691	266
HP0691	268
HP1198	270
HP1198	272
HP0073	274
HP0073	276
HP0073	278

Table III :

Bait polypeptides (ORF reference according to Tomb et al.)	SID ® Nucleic acid sequence (SEQ ID N°)
HP0868	1
HP0868	3
HP0868	5
HP0868	7
HP0800	9
HP0800	11
HP0800	13
HP0800	15
HP0800	17
HP0800	19
HP0800	21
HP0801	23
HP0801	25
HP0801	27
HP0887	29
HP0887	31
HP0887	33
HP0887	35
HP0887	37
HP0887	39
HP0887	41
HP0289	43
HP0289	45
HP0289	47
HP0289	49
HP0289	51
HP0289	53

HP0289	55
HP0289	57
HP0289	59
HP0289	61
HP0068	63
HP0068	65
HP0047	67
HP0047	69
HP0047	71
HP0069	73
HP0066	75
HP0268	77
HP1293	79
HP0061	81
HP0061	83
HP0061	85
HP0064	87
HP1198	89
HP1198	91
HP1198	93
HP1198	95
HP1198	97
HP1198	99
HP1198	101
HP1198	103
HP1198	105
HP1198	107
HP1198	109
HP1198	111
HP1198	113
HP1198	115

HP1198	117
HP1231	119
HP1032	121
HP1032	123
HP1032	125
HP1032	127
HP1032	129
HP1230	131
HP1230	133
HP1529	135
HP0978	137
HP0978	139
HP0071	141
HP0071	143
HP0071	145
HP0071	147
HP0071	149
HP0071	151
HP0073	153
HP0073	155
HP0073	157
HP0935	159
HP0935	161
HP0935	163
HP0338	165
HP0338	167
HP1246	169
HP1246	171
HP1246	173
HP1246	175
HP1246	177

HP1246	179
HP1246	181
HP0797	183
HP0797	185
HP0797	187
HP0797	189
HP0797	191
HP0311	193
HP0067	195
HP0067	197
HP0067	199
HP0067	201
HP0067	203
HP1244	205
HP1244	207
HP1067	209
HP0875	211
HP0776	213
HP0776	215
HP0776	217
HP0776	219
HP0697	221
HP0697	223
HP0697	225
HP0697	227
HP0697	229
HP0697	231
HP0697	233
HP0697	235
HP0697	237
HP0697	239

HP0887	241
HP0887	243
HP0887	245
HP0887	247
HP1247	249
HP1247	251
HP0874	253
HP0072	255
HP0391	257
HP0391	259
HP0070	261
HP0070	263
HP0691	265
HP0691	267
HP1198	269
HP1198	271
HP0073	273
HP0073	275
HP0073	277

Claims

1. A method for producing a collection of recombinant cell clones usable for two-hybrid systems comprising the steps of :

a) fragmenting DNA ;

b) inserting polynucleotidic fragments obtained in step a) in plasmids in such a way that the expression of said plasmids in host cell leads to an hybrid polypeptide containing a specific domain capable of activating a reporter gene when associated with a complementary domain ;

c) transforming cell clones with plasmids obtained in step b) ; and

d) optionally, selecting the transformed recombinant cell clones obtained in step c) ;

wherein DNA of step a) is genomic DNA obtained from a prokaryotic micro-organism.

2. A method according to claim 1, wherein the step a) of fragmenting DNA is carried by a nebulization process.

3. A method according to claim 1 or 2, wherein the prokaryotic micro-organism is *Helicobacter pylori.*

4. A method according claim 1 or 2, wherein the prokaryotic micro-organism is *Staphylococcus aureus.*

5. A method according claim 1 or 2, wherein the prokaryotic micro-organism is *Streptococcus pneumoniae.*

6. A method according claim 1 or 2, wherein the prokaryotic micro-organism is *Escherichia coli.*

7. Collection of recombinant cell clones usable for two-hybrid systems obtainable by a method according to anyone of claims 1 to 6.

8. Collection of recombinant cell clones usable for two-hybrid systems, each recombinant cell clone containing a polynucleotide inserted in a plasmid whose expression leads to hybrid polypeptide containing a specific domain, wherein the said polynucleotide is a genomic DNA fragment obtained from a prokaryotic micro-organism.

9. Collection of recombinant cell clones usable for two-hybrid systems according to claim 8 wherein said genomic DNA fragment is obtained by a fragmentation process by nebulization.

10. Collection of recombinant cell clones according to anyone of claims 7 to 9, wherein the prokaryotic micro-organism is *Helicobacter pylori*.

11. Collection of recombinant cell clones according to anyone of claims 7 to 9, wherein the prokaryotic micro-organism is *Staphylococcus aureus*.

12. Collection of recombinant cell clones according to anyone of claims 7 to 9, wherein the prokaryotic micro-organism is *Streptococcus pneumoniae*.

13. Collection of recombinant cell clones according to anyone of claims 7 to 9, wherein the prokaryotic micro-organism is *Escherichia coli*.

14. Collection of recombinant cell clones according to anyone of claims 7 to 13, wherein the recombinant cell clones are selected from the group consisting of Gram+ or Gram- bacteria, yeasts, fungi and mammalian cells.

15. Collection of recombinant cell clones according to claim 14, wherein the recombinant cell clones are selected from the group consisting of *Escherichia coli* bacteria and *Saccharomyces cerevisiae* yeast.

16. Collection of recombinant cell clones according to claim 15, wherein the recombinant cell clones are *E. coli* bacteria.

17. Collection of recombinant cell clones according to anyone of claims 7 to 16, wherein the plasmids comprise at least a nucleic sequence coding a promoter, a specific domain, a multicloning site where the said polypeptide is cloned, and a selection marker.

18. Collection of recombinant cell clones according to anyone of claims 7 to 17, wherein the polynucleotide is inserted in the plasmid pACTIIst or pP6.

19. Collection of recombinant cell clones according to claim 18, wherein the collection contains 10^6 to 10^7 recombinant *Escherichia coli* clones and wherein the proportion of different cell clones with insert is at least 60 %.

20. Collection of recombinant cell clones according to claim 18 or 19 filed with CNCM on April 13, 1999 under number I-2181.

21. Collection of recombinant cell clones according to claim 18 or 19 filed with CNCM on March 23, 2000 under number I-2416.

22. Collection of recombinant cell clones according to claim 18 or 19 filed with CNCM on March 23, 2000 under number I-2414.

23. Collection of recombinant cell clones according to claim 18 or 19 filed with CNCM on March 23, 2000 under number I-2415.

24. Collection of recombinant cell clones according to claim 18 or 19 filed with CNCM on March 23, 2000 under number I-2417.

25. Collection of recombinant cell clones according to claim 18, wherein the collection contains 10^5 to 1.5 x 10^6 haploid recombinant Saccharomyces *cerevisiae* clones and wherein the proportion of different cell clones with insert is at least 60 %.

26. Collection of recombinant cell clones according to claim 18 or 25 filed with CNCM on April 13, 1999 under number I-2182.

27. Collection of recombinant cell clones according to claim 18 or 25 filed with CNCM on March 23, 2000 under number I-2420.

28. Collection of recombinant cell clones according to claim 18 or 25 filed with CNCM on March 23, 2000 under number I-2419.

29. Collection of recombinant cell clones according to claim 18 or 25 filed with CNCM on March 23, 2000 under number I-2418.

30. Collection of recombinant cell clones according to anyone of claims 7 to 17, wherein the polynucleotide is inserted in the plasmid pAS2ΔΔ.

31. Collection of recombinant cell clones according to anyone of claims 7 to 17, wherein the polynucleotide is inserted in a plasmid selected from the group consisting of pT25, pKT25, pUT18 and pUT18C.

32. Kit for screening protein-protein interaction comprising a collection of recombinant cell clones usable for two-hybrid systems according to anyone of claims 7 to 31.

33. A yeast two-hybrid system method for identifying a recombinant cell clone containing a prey polynucleotide encoding a prey polypeptide capable of interacting with a bait polypeptide comprising the steps of :

a) mating at least one first haploid recombinant cell clone of a collection of recombinant cell clones according to claim 25 or 26 transformed with a plasmid containing the prey polynucleotide to be assayed with a second haploid recombinant *S. cerevisiae* cell clone transformed with a plasmid containing a bait polynucleotide encoding said bait polypeptide ;

b) cultivating diploid cell obtained in step a) on selective medium ; and

c) selecting recombinant cell clones capable of growing on selective medium.

34. A yeast two-hybrid system method for identifying a prey polynucleotide encoding a prey polypeptide capable of interacting with a bait polypeptide comprising the steps of :

a) identifying a recombinant cell clone containing a prey polynucleotide encoding a prey polypeptide capable of interacting with a bait polypeptide according to claim 33 ; and

b) characterizing the prey polynucleotide contained in each recombinant cell clone selected in step a).

35. A bacterial two-hybrid system method for identifying a recombinant cell clone containing a prey polynucleotide encoding a prey polypeptide capable of interacting with a bait polypeptide comprising the steps of :

a) transforming bacterial cell clones with a plasmid containing a bait polynucleotide encoding said bait polypeptide ;

b) rescuing prey plasmids containing prey polynucleotides from the collection according to claims 7 to 31 ;

c) transforming the recombinant bacterial cell clones obtained in step a) with the plasmid rescued in step b) ;

d) cultivating bacterial recombinant cells obtained in step c) on selective medium ;

e) selecting recombinant cell clones capable of growing on selective medium.

36. A bacterial two-hybrid system method for identifying a prey polynucleotide encoding a prey polypeptide capable of interacting with a bait polypeptide comprising the steps of :

a) identifying a bacterial recombinant cell clone containing a prey polynucleotide encoding a prey polypeptide capable of interacting with a bait polypeptide according to claim 35 ; and

b) characterizing the prey polynucleotide contained in each recombinant cell clone selected in step a).

37. Method according to anyone of claims 33 to 36, wherein the bait polypeptide is a human polypeptide.

38. Method according to anyone of claims 33 to 36, wherein the bait polypeptide is a *Helicobacter pylori* polypeptide.

39. Method according to anyone of claims 33 to 36, wherein the bait polypeptide is a *Staphylococcus aureus* polypeptide.

40. Method according to anyone of claims 33 to 36, wherein the bait polypeptide is a *Streptococcus pneumoniae* polypeptide.

41. Method according to anyone of claims 33 to 36, wherein the bait polypeptide is a *Escherichia coli* polypeptide.

42. A recombinant diploid yeast cell obtained by step a) of the method according to claim 33.

43. A recombinant diploid yeast cell obtained by the method according to claim 33.

44. A set of two purified or isolated polynucleotides consisting of a first polynucleotide, or fragment thereof, encoding a prey polypeptide capable of interacting with a bait polypeptide and a second polynucleotide, or a fragment thereof having at least 12 consecutive nucleotides, encoding said bait polypeptide wherein the prey polynucleotide is identified by a method according to anyone of claims 34 and 36.

45. A set of two purified or isolated polypeptides encoded by the set of two polynucleotides according to claim 44.

46. Protein-protein interaction wherein the two interacting proteins consist of a set of two polypeptides according to claim 45.

47. Protein-protein interaction according to claim 46, wherein the set of two polypeptides consists of two *Helicobacter pylori* polypeptides.

48. Protein-protein interaction according to claim 46, wherein the set of two polypeptides consists of two *Staphylococcus aureus* polypeptides.

49. Protein-protein interaction according to claim 46, wherein the set of two polypeptides consists of two *Streptococcus pneumoniae* polypeptides.

50. Protein-protein interaction according to claim 46, wherein the set of two polypeptides consists of two *Escherichia coli* polypeptides.

51. Isolated complex comprising at least the two polypeptides encoded by the set of two polynucleotides according to claim 44.

52. Isolated complex according to claim 51, characterized in that said complex comprises at least a polypeptide encoded by the ORF HP1198 and a polypeptide encoded by the ORF HP1293.

53. Isolated complex according to claim 51, characterized in that said complex comprises at least a polypeptide encoded by the ORF HP1198 and a polypeptide encoded by the ORF HP0088.

54. Isolated complex according to claim 51, characterized in that said complex comprises at least a polypeptide encoded by the ORF HP1198 and a polypeptide encoded by the ORF HP1032.

55. A computable readable medium having stored thereon protein-protein interactions according to claim 46 to 50.

56. A computable readable medium according to claim 55, wherein the protein-protein interactions stored thereon is stored in a form of a map.

57. A computable readable medium according to claim 55 or 56, wherein the protein-protein interactions stored thereon are linked to annotated database through Internet.

58. A method for identifying a polynucleotide encoding a selecting interacting domain (SID®) of a prey polypeptide of interest from a prokaryotic micro-organism capable of interacting with a bait polypeptide comprising the steps of :

a) selecting from prey polynucleotides identifyied by a method according to claim 34 or 36 all prey polynucleotides encoding a polypeptide capable of interacting with said bait polypeptide and containing a nucleic acid fragment identical to a nucleic fragment of the polynucleotide encoding the prey polypeptide of interest ;

b) determining the polynucleotide common to said all prey polynucleotides selected in step a) ; and

c) identifying the polynucleotide determining in step b) as being the polynucleotide encoding the selected interacting domain (SID®) of said prey polypeptide of interest.

59. Purified or isolated polynucleotide encoding a selecting interacting domain (SID®) of a prey polypeptide of interest from a prokaryotic micro-organism capable of interacting with a bait polypeptide obtainable by a method according to claim 58.

60. Purified or isolated polynucleotide according to claim 59 selected from the group consisting of :

a) a polynucleotide encoding an amino acids sequence identified by the reference indicated in the right column "SID®" in table II ;

b) a polynucleotide having the sequence identified by the reference indicated in the right column "SID®" in table III ;

c) fragment having at least 12 consecutive nucleotides of polynucleotide of a) or b), complement thereof, and RNA corresponding to said polynucleotide ; and

d) a polynucleotide having at least 80 % identity degree after alignment to a nucleic acid sequence of a polynucleotide of a) or b).

61. Purified or isolated polypeptide selected from the group consisting of :

a) a polypeptide having an amino acids sequence identified by the reference indicated in the right column "SID®" in table II, and fragment thereof having at least 5 consecutive amino acids ; and

b) a polypeptide encoded by a polynucleotide according to claim 59 or 60.

62. Use of a polynucleotide according to claim 60 as a primer for amplification.

63. Use of a polynucleotide according to claim 60 as a specific probe for detection.

64. Cloning or expression vector containing a polynucleotide according to anyone of claims 59 and 60.

65. Vector according to claim 64, wherein the vector is the plasmid pACTIIst, pAS2ΔΔ or pP6.

66. Vector according to claim 64, wherein the vector is the plasmid selected from the group consisting of pT25, pKT25, pUT18 and pUT18C.

67. Vector according to claim 64, wherein the vector is self replicated.

68. Vector according to claim 64 or 67, wherein the vector is a viral vector.

69. Vector according to claim 68, wherein the vector is chosen between an adenovirus, AAV, a retrovirus, a proxivirus or an herpes virus.

70. Vector according to anyone of claims 64 to 69 including elements allowing expression and/or secretion of said polynucleotide in a host cell.

71. Host cell transformed with a vector according to anyone of claims 64 to 70.

72. Host cell according to claim 71, wherein the host cell is a prokaryotic cell.

73. Host cell according to claim 71, wherein the host cell is an eukaryotic cell.

74. Method for producing a polypeptide according to anyone of claims 45 and 61, comprising the steps of :

a) cultivating a host cell according to anyone of claims 71 to 73 under conditions and in culture medium allowing the growth of said host cell and the expression of said polypeptide; and

b) recovering said polypeptide directly from the culture medium or from said cultivated cell obtained in step a).

75. Purified or isolated polypeptide obtained by the method according to claim 74.

76. A method for selecting an agent capable of modulating the protein-protein interaction of a step of two polypeptides according to claim 45 comprising the steps of :

a) cultivating a recombinant cell clone containing a reporter gene expression of which is toxic for said recombinant cell clone and transformed with two plasmids wherein :

i) the first plasmid contains a nucleic construct comprising a nucleic sequence encoding a first hybrid polypeptide containing one of said two polypeptides and a DNA binding domain ;

ii) the second plasmid contains a nucleic construct comprising a nucleic sequence encoding a second hybrid polypeptide containing the second of said two polypeptides and an activating domain capable of activating said toxic reporter gene when the first and the second hybrid polypeptides are interacting ;

on a selective medium containing the agent to be tested and allowing the growth of said recombinant cell clone when the toxic reporter gene is not activated ; and

b) selecting agent which is capable of inhibiting the growth of the recombinant cell clone cultivated in step a).

77. A method for selecting an agent capable of modulating the protein-protein interaction of a set of two polypeptides according to claim 45 comprising the steps of :

a) cultivating a permeable recombinant cell clone containing a reporter gene expression of which is toxic for said recombinant cell clone and transformed with two plasmids wherein :

i) the first plasmid contains a nucleic construct comprising a nucleic sequence encoding a first hybrid polypeptide containing one of said two polypeptides and the first domain of an enzyme ;

ii) the second plasmid contains a nucleic construct comprising a nucleic sequence encoding a second hybrid polypeptide containing the second of said two polypeptides and the second part of said enzyme capable of activating said toxic reporter gene when the first and the second hybrid polypeptides are interacting, said interaction restoring the activity of the enzyme ;

on a selective medium containing the agent to be tested and allowing the growth of said recombinant cell clone when the toxic reporter gene is not activated ; and

b) selecting agent which is capable of inhibiting the growth of the recombinant cell clone cultivated in step a).

78. A method according to claim 77, for selecting an agent capable of modulating the interaction between a polypeptide encoded by the ORF HP1198, or a fragment or homologuous polypeptide thereof, and a polypeptide encoded by the ORF HP1293, or a fragment or homologuous polypeptide thereof.

79. A method according to claim 77, for selecting an agent capable of modulating the interaction between a polypeptide encoded by the ORF HP1198, or a fragment or homologuous polypeptide thereof, and a polypeptide encoded by the ORF HP0088, or a fragment thereof or homologuous polypeptide thereof.

80. A method according to claim 77, for selecting an agent capable of modulating the interaction between a polypeptide encoded by the ORF HP1198, or a fragment or homologuous polypeptide thereof, and a polypeptide encoded by the ORF HP1032, or a fragment or homologuous polypeptide thereof.

81. Modulator agent selected by the method according to claim 76 or 77.

82. Kit for screening a modulator agent comprising at least one recombinant transformed cell clone according to step a) of claim 76 or 77.

83. Use of a polypeptide according to anyone of claims 45 and 61 for the modulation of *Helicobacter pylori*'s protein interaction.

84. Method for the production of monoclonal or polyclonal comprising the step of immunization of an animal or human organism with an immunogenic agent comprising a polypeptide according to anyone of claims 45 and 61, a vector according to anyone of claims 65 to 70 or a host cell according to anyone of claims 71 to 73.

85. Antibody obtained by the method according to claim 84.

86. A pharmaceutical composition comprising a compound selected from the group consisting of :

a) a polynucleotide according to anyone of claims 59 and 60 ;

b) a polypeptide according to anyone of claims 45 and 61 ;

c) a vector according to anyone of claims 62 to 70 ;

d) a host cell according to anyone of claims 71 to 73 ;

e) a modulator agent according to claim 80 ; and

f) an antibody according to claim 85.

87. A pharmaceutical composition according to claim 86, wherein said composition is administered by any route such as intravenous route, intramuscular route, oral route, or mucosal route with an acceptable physiological carrier and/or adjuvant.

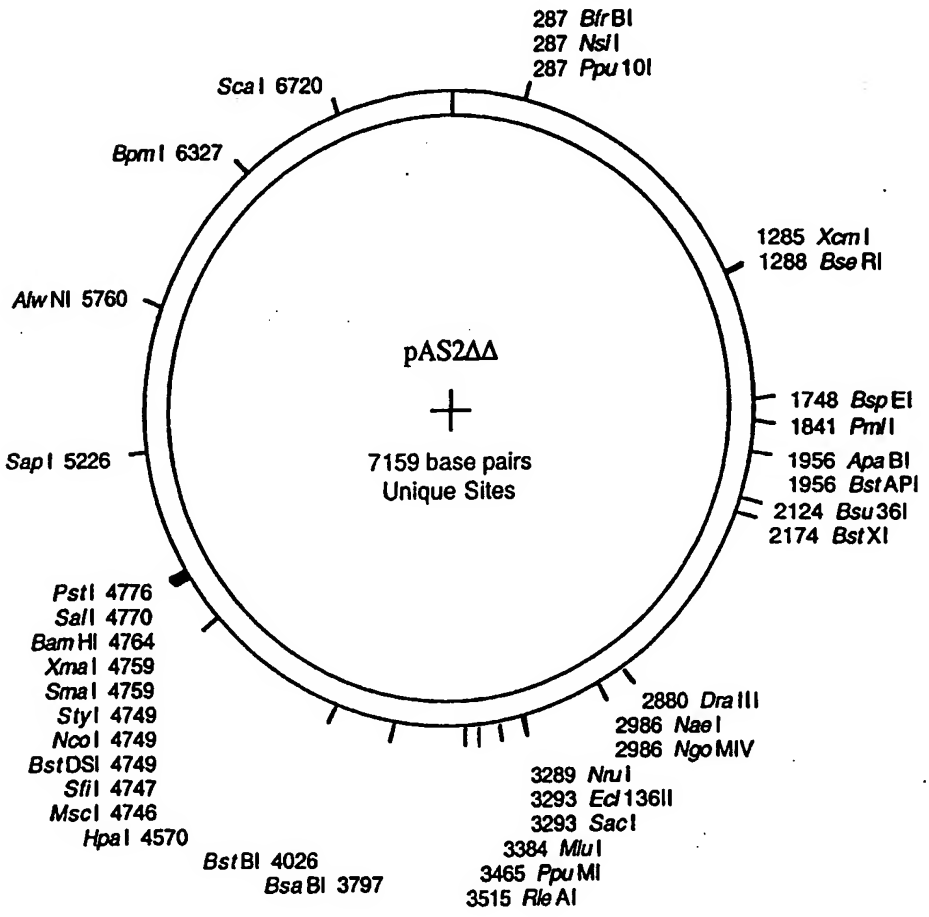

287 BfrBI
287 NsiI
287 Ppu10I
ScaI 6720
BpmI 6327
1285 XcmI
1288 BseRI
AlwNI 5760
pAS2ΔΔ
1748 BspEI
1841 PmlI
7159 base pairs
Unique Sites
SapI 5226
1956 ApaBI
1956 BstAPI
2124 Bsu36I
2174 BstXI
PstI 4776
SalI 4770
BamHI 4764
XmaI 4759
SmaI 4759
StyI 4749
NcoI 4749
BstDSI 4749
SfiI 4747
MscI 4746
HpaI 4570
2880 DraIII
2986 NaeI
2986 NgoMIV
3289 NruI
3293 Ecl136II
3293 SacI
3384 MluI
3465 PpuMI
3515 RleAI
BstBI 4026
BsaBI 3797

FIGURE 1

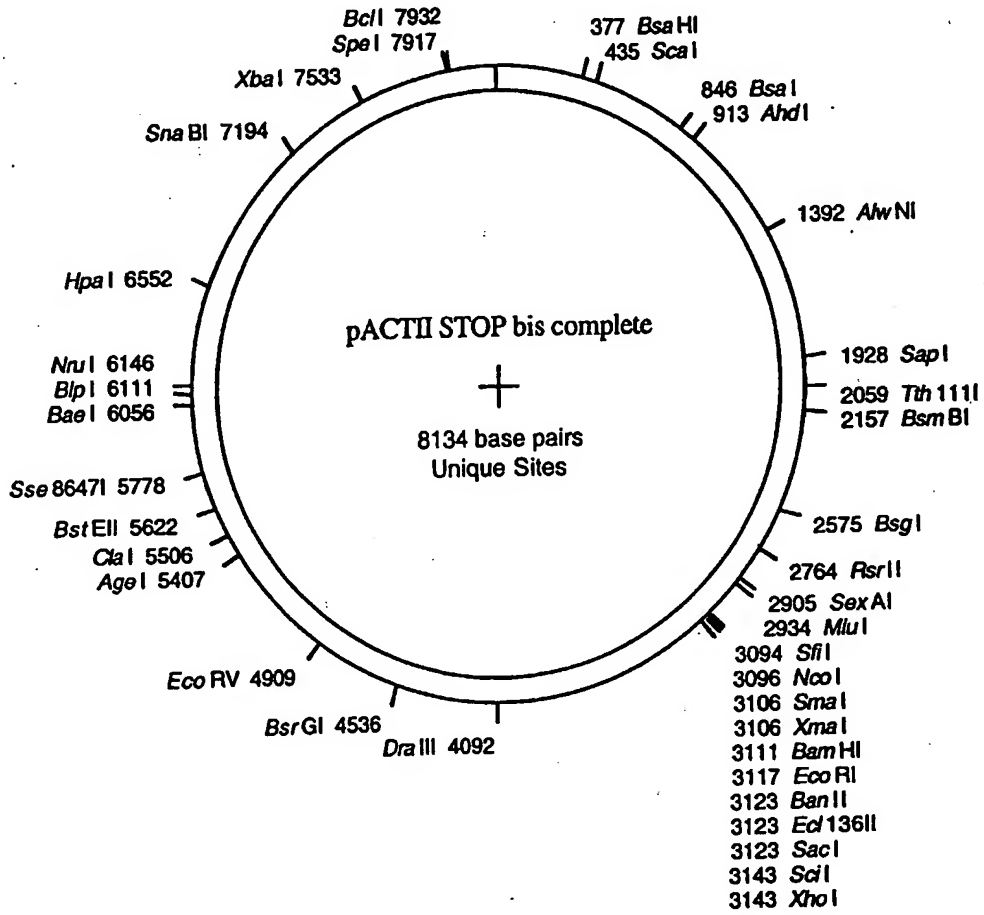

pACTII STOP bis complete
8134 base pairs
Unique Sites
BclI 7932
SpeI 7917
XbaI 7533
SnaBI 7194
HpaI 6552
NruI 6146
BlpI 6111
BaeI 6056
Sse8647I 5778
BstEII 5622
ClaI 5506
AgeI 5407
EcoRV 4909
BsrGI 4536
DraIII 4092
377 BsaHI
435 ScaI
846 BsaI
913 AhdI
1392 AlwNI
1928 SapI
2059 Tth111I
2157 BsmBI
2575 BsgI
2764 RsrII
2905 SexAI
2934 MluI
3094 SfiI
3096 NcoI
3106 SmaI
3106 XmaI
3111 BamHI
3117 EcoRI
3123 BanII
3123 Ecl136II
3123 SacI
3143 SclI
3143 XhoI

FIGURE 2

VECTORS TO CREATE FUSED PROTEINS WITH T18 FRAGMENT

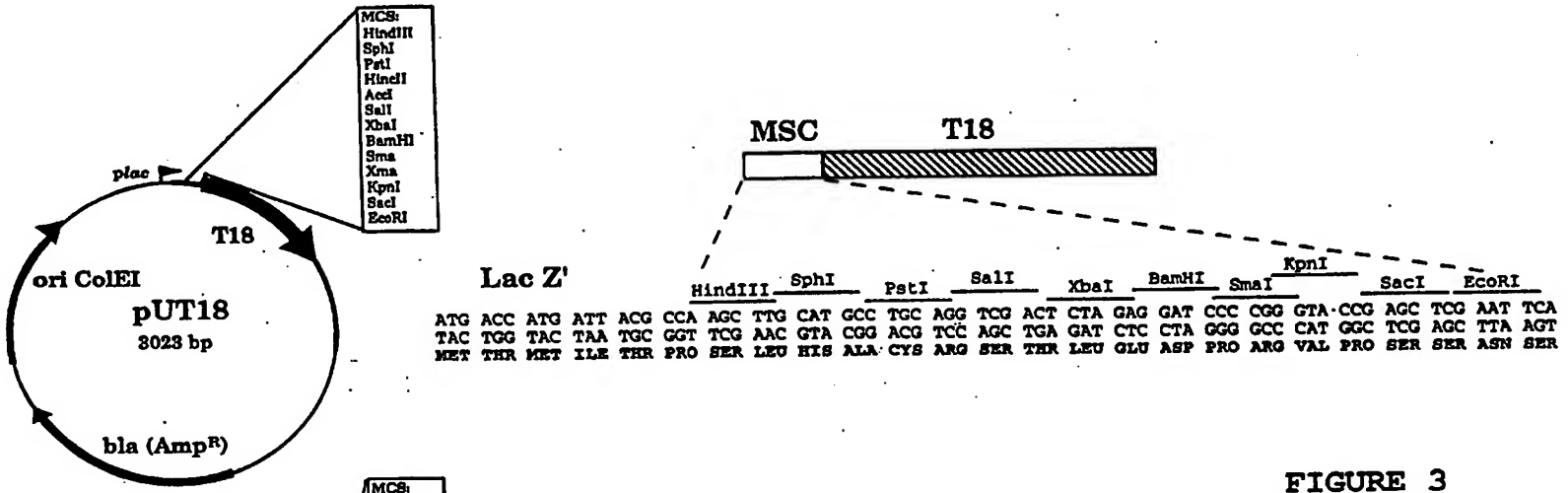


FIGURE 3

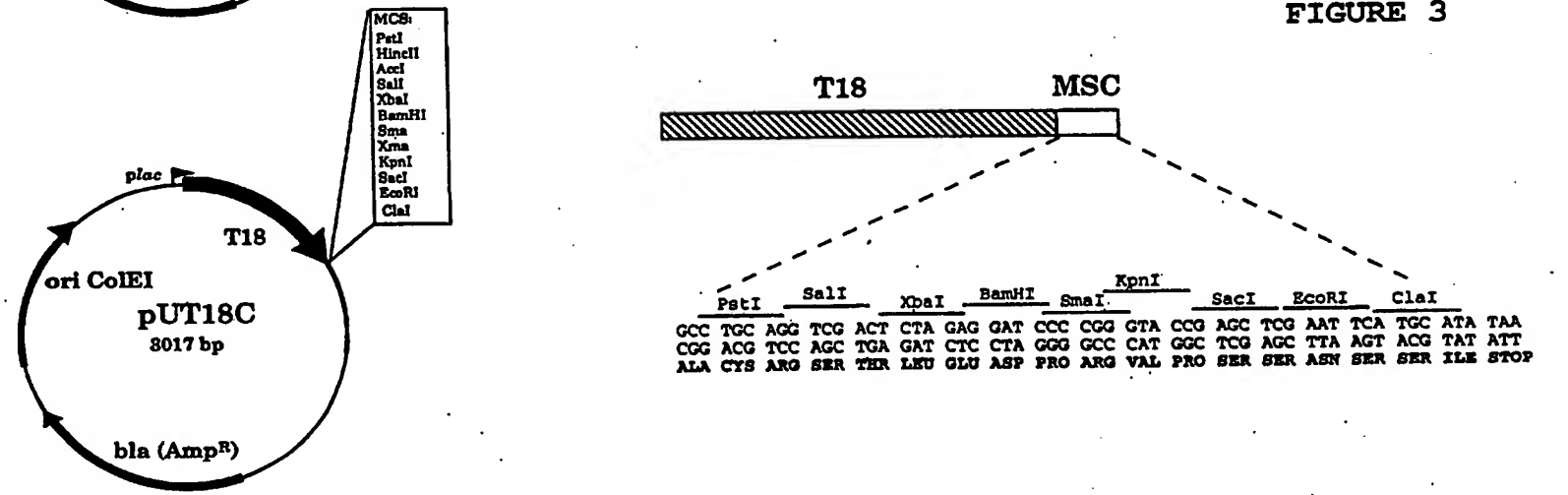
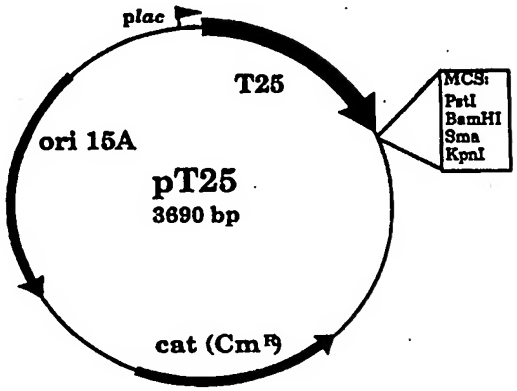
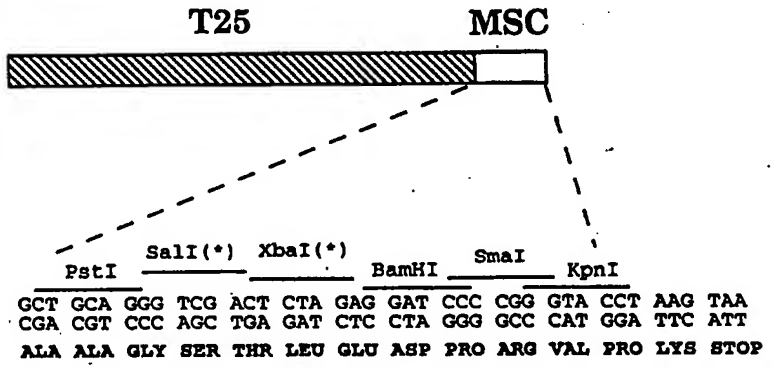


FIGURE 4

VECTORS TO CREATE FUSED PROTEINS WITH T25 FRAGMENT

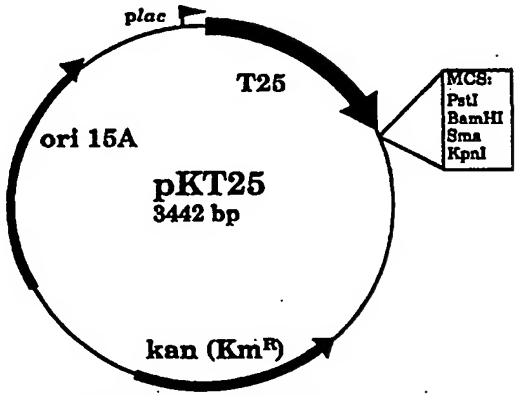


Derivative of pACYC184

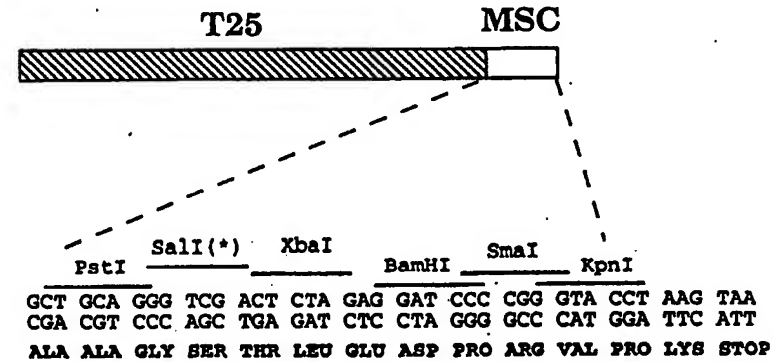


(*) Restriction sites are not unique

FIGURE 5



Derivative of pSU40



(*) Restriction site is not unique

FIGURE 6

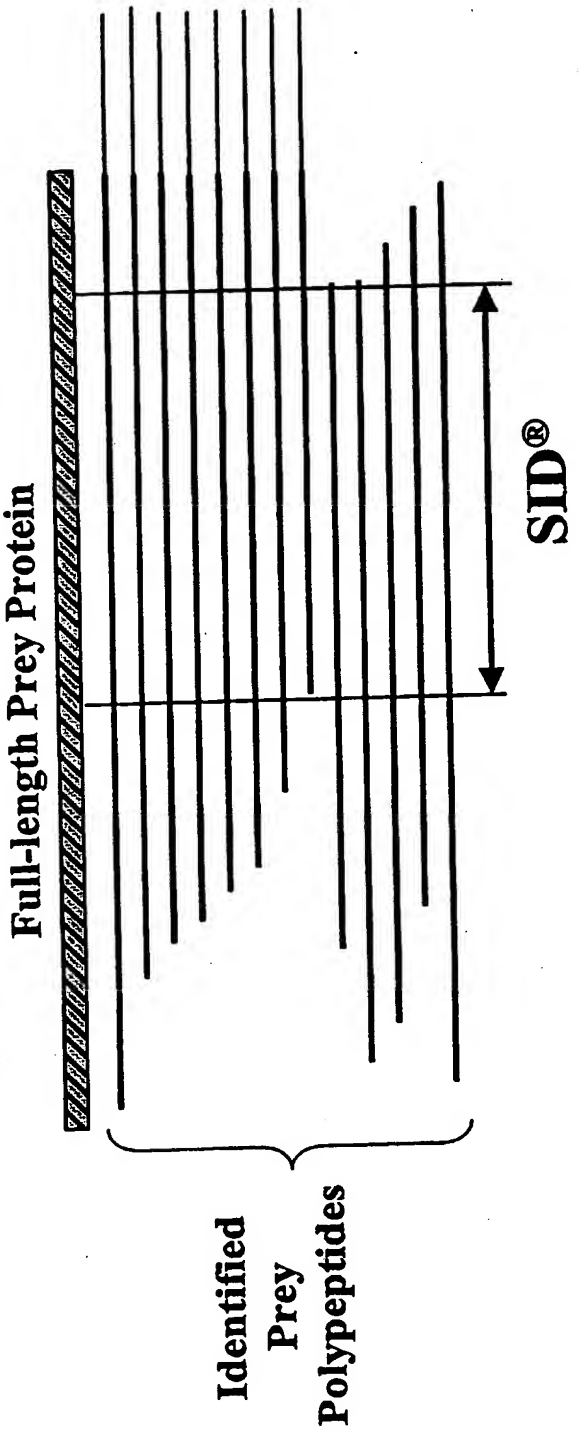
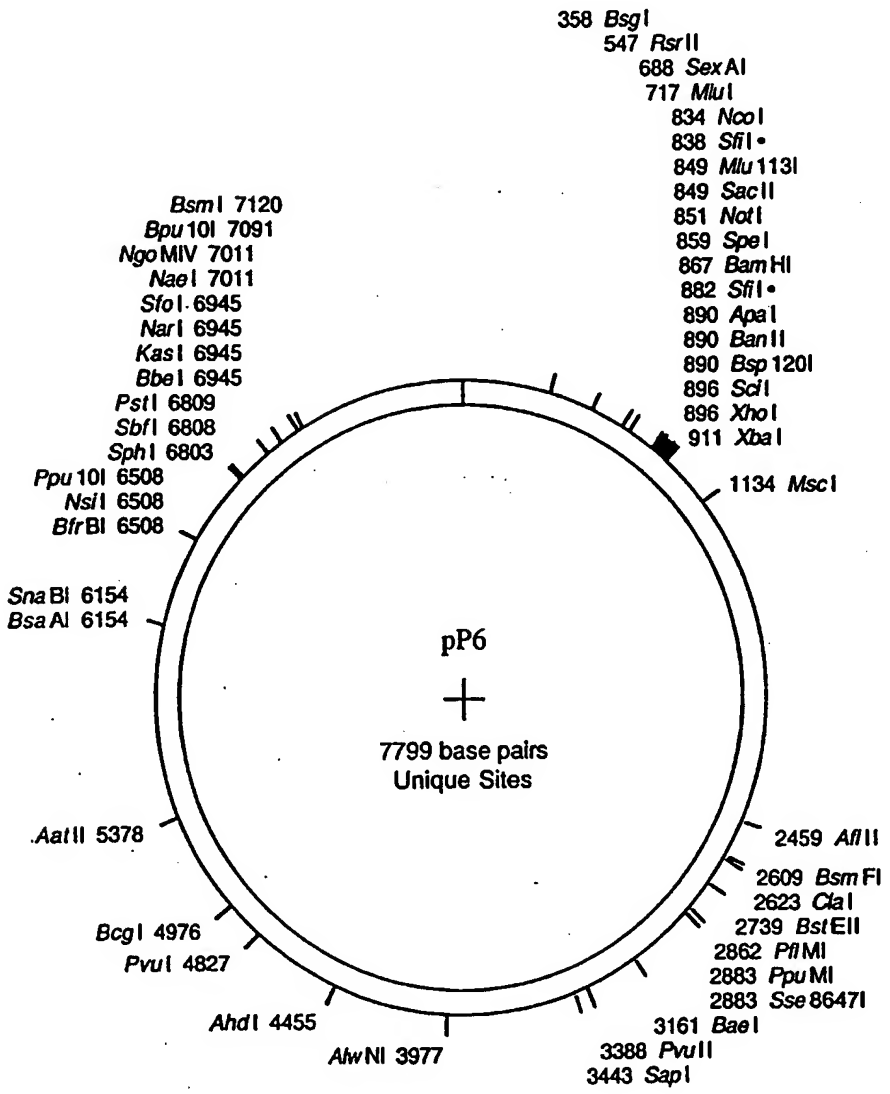

Full-length Prey Protein
SID®
Identified
Prey
Polypeptides

FIGURE 7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688 SexAI
717 MluI
834 NcoI
838 SfiI•
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849 SacII
851 NotI
859 SpeI
867 BamHI
882 SfiI•
890 ApaI
890 BanII
890 Bsp120I
896 SclI
896 XhoI
911 XbaI
1134 MscI
2459 AflII
2609 BsmFI
2623 ClaI
2739 BstEII
2862 PflMI
2883 PpuMI
2883 Sse8647I
3161 BaeI
3388 PvuII
3443 SapI
AlwNI 3977
AhdI 4455
Pvu I 4827
BcgI 4976
AatII 5378
BsaAI 6154
SnaBI 6154
BfrBI 6508
NsiI 6508
Ppu10I 6508
SphI 6803
SbfI 6808
PstI 6809
BbeI 6945
KasI 6945
NarI 6945
SfoI 6945
NaeI 7011
NgoMIV 7011
Bpu10I 7091
BsmI 7120
pP6
7799 base pairs
Unique Sites

FIGURE 8

SEQUENCE LISTING

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<150> EP 99401066.8
<151> 1999-04-30
<160> 278
<170> PatentIn Ver. 2.1

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gct gaa gaa gtg ggg ctt tcg tta gat aaa gtg aag aat gtg att aag   96
Ala Glu Glu Val Gly Leu Ser Leu Asp Lys Val Lys Asn Val Ile Lys
             20                  25                  30

gtg act aaa gag cct atc agt ttg gaa acc cca gtc ggc aat gat gat  144
Val Thr Lys Glu Pro Ile Ser Leu Glu Thr Pro Val Gly Asn Asp Asp
         35                  40                  45

gat ggc aag ttt ggg gat ttc gtg gaa gat aag aat atc gtc agc tcc  192
Asp Gly Lys Phe Gly Asp Phe Val Glu Asp Lys Asn Ile Val Ser Ser
     50                  55                  60

att gat cac atc atg cga gaa gat ttg aaa gca caa att gaa agc gtt  240
Ile Asp His Ile Met Arg Glu Asp Leu Lys Ala Gln Ile Glu Ser Val
 65                  70                  75                  80

ttg gat cag ttg aat gag cga gaa aaa gcg gtg atc cgc atg cgt ttt  288
Leu Asp Gln Leu Asn Glu Arg Glu Lys Ala Val Ile Arg Met Arg Phe
                 85                  90                  95

ggg ctt tta gac gat gaa agc gat cga act tta gaa gaa att ggc aag  336
Gly Leu Leu Asp Asp Glu Ser Asp Arg Thr Leu Glu Glu Ile Gly Lys
            100                 105                 110

gaa ttg aat gtt act aga gaa agg gtg cgc cag att gaa agc tct gcg  384
Glu Leu Asn Val Thr Arg Glu Arg Val Arg Gln Ile Glu Ser Ser Ala
        115                 120                 125

att aaa aaa ttg aga agc ccg cag tac ggg cgc att tta aga aac tat  432
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    130                 135                 140

ttg cgc att                                                     441
Leu Arg Ile
145
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             20                  25                  30

Val Thr Lys Glu Pro Ile Ser Leu Glu Thr Pro Val Gly Asn Asp Asp
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```
         35                  40                  45
Asp Gly Lys Phe Gly Asp Phe Val Glu Asp Lys Asn Ile Val Ser Ser
     50                  55                  60
Ile Asp His Ile Met Arg Glu Asp Leu Lys Ala Gln Ile Glu Ser Val
 65                  70                  75                  80
Leu Asp Gln Leu Asn Glu Arg Glu Lys Ala Val Ile Arg Met Arg Phe
                 85                  90                  95
Gly Leu Leu Asp Asp Glu Ser Asp Arg Thr Leu Glu Glu Ile Gly Lys
            100                 105                 110
Glu Leu Asn Val Thr Arg Glu Arg Val Arg Gln Ile Glu Ser Ser Ala
        115                 120                 125
Ile Lys Lys Leu Arg Ser Pro Gln Tyr Gly Arg Ile Leu Arg Asn Tyr
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Leu Arg Ile
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  1               5                  10                  15
gtt ggc tct atc act aaa atc aat ttt ttt cat aag cat ggg tat ttg   96
Val Gly Ser Ile Thr Lys Ile Asn Phe Phe His Lys His Gly Tyr Leu
             20                  25                  30
ggg att tat aaa aac cct ttt ttg aaa aat ggg gga gaa acg att tta   144
Gly Ile Tyr Lys Asn Pro Phe Leu Lys Asn Gly Gly Glu Thr Ile Leu
         35                  40                  45
aaa gcc ttg gaa ttt atc gct ttt gaa gag ttc caa tta cat tct ttg   192
Lys Ala Leu Glu Phe Ile Ala Phe Glu Glu Phe Gln Leu His Ser Leu
     50                  55                  60
cat tta gaa gtg atg gaa aac aat ttc aaa gcg atc gct ttt tat gaa   240
His Leu Glu Val Met Glu Asn Asn Phe Lys Ala Ile Ala Phe Tyr Glu
 65                  70                  75                  80
aaa aac cat tat gag tta gag ggg cgt ttg aaa ggc ttt att tct aaa   288
Lys Asn His Tyr Glu Leu Glu Gly Arg Leu Lys Gly Phe Ile Ser Lys
                 85                  90                  95
gat aag gag ttt ata gac gtt ctt ttg tat tat aag gat aag aaa gga   336
Asp Lys Glu Phe Ile Asp Val Leu Leu Tyr Tyr Lys Asp Lys Lys Gly
            100                 105                 110
tat aat gat caa tct ctt cta aaa ctt                              363
Tyr Asn Asp Gln Ser Leu Leu Lys Leu
        115                 120
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Val Gly Ser Ile Thr Lys Ile Asn Phe Phe His Lys His Gly Tyr Leu
             20                  25                  30
Gly Ile Tyr Lys Asn Pro Phe Leu Lys Asn Gly Gly Glu Thr Ile Leu
         35                  40                  45
Lys Ala Leu Glu Phe Ile Ala Phe Glu Glu Phe Gln Leu His Ser Leu
     50                  55                  60
His Leu Glu Val Met Glu Asn Asn Phe Lys Ala Ile Ala Phe Tyr Glu
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65 70 75 80
Lys Asn His Tyr Glu Leu Glu Gly Arg Leu Lys Gly Phe Ile Ser Lys
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Asp Lys Glu Phe Ile Asp Val Leu Leu Tyr Tyr Lys Asp Lys Lys Gly
100 105 110
Tyr Asn Asp Gln Ser Leu Leu Lys Leu
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att atc act caa ggc aat gaa atg cgt ttg ttg tct tta gaa atg tta 96
Ile Ile Thr Gln Gly Asn Glu Met Arg Leu Leu Ser Leu Glu Met Leu
20 25 30
gcg gaa 102
Ala Glu

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20 25 30
Ala Glu

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<213> Helicobacter pylori
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Met Glu Asp Tyr Ala Ser Arg Thr Ala Gly Ala Leu Glu Arg Leu Asp
1 5 10 15
aag att gtt gaa aca gaa cag aag aat caa caa act aaa ttg gac aca 96
Lys Ile Val Glu Thr Glu Gln Lys Asn Gln Gln Thr Lys Leu Asp Thr
20 25 30
gaa aat ttg aaa ata att att gaa act ttg aga agt aaa atc aat ggg 144
Glu Asn Leu Lys Ile Ile Ile Glu Thr Leu Arg Ser Lys Ile Asn Gly
35 40 45
aat cag caa aag atg ctt gat aaa agt aaa gaa atg agc aga aat ttt 192
Asn Gln Gln Lys Met Leu Asp Lys Ser Lys Glu Met Ser Arg Asn Phe
50 55 60
aag ctt gat agc act aaa aac gag ata gac gca att aaa gat ttg att 240
Lys Leu Asp Ser Thr Lys Asn Glu Ile Asp Ala Ile Lys Asp Leu Ile
65 70 75 80
aaa aag gct aat gag caa ata gcc aat tat aat gag atg ata aag gat 288
Lys Lys Ala Asn Glu Gln Ile Ala Asn Tyr Asn Glu Met Ile Lys Asp
85 90 95
att gaa aaa cag aaa aag agt tgt aag gaa caa act tgg aaa ttt cta 336

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Ile Glu Lys Gln Lys Lys Ser Cys Lys Glu Gln Thr Trp Lys Phe Leu
            100                 105                 110
gtc aat gaa ttt aaa agt gat ata caa gaa tat aat aaa aag tat tgc   384
Val Asn Glu Phe Lys Ser Asp Ile Gln Glu Tyr Asn Lys Lys Tyr Cys
        115                 120                 125
ggt ttg gag aaa gga ata aac aat tta gag aaa gca att agt gaa aat   432
Gly Leu Glu Lys Gly Ile Asn Asn Leu Glu Lys Ala Ile Ser Glu Asn
    130                 135                 140
caa gaa gag gta aag aaa tta gaa aat gaa                           462
Gln Glu Glu Val Lys Lys Leu Glu Asn Glu
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Lys Ile Val Glu Thr Glu Gln Lys Asn Gln Gln Thr Lys Leu Asp Thr
            20                  25                  30
Glu Asn Leu Lys Ile Ile Ile Glu Thr Leu Arg Ser Lys Ile Asn Gly
        35                  40                  45
Asn Gln Gln Lys Met Leu Asp Lys Ser Lys Glu Met Ser Arg Asn Phe
    50                  55                  60
Lys Leu Asp Ser Thr Lys Asn Glu Ile Asp Ala Ile Lys Asp Leu Ile
65                  70                  75                  80
Lys Lys Ala Asn Glu Gln Ile Ala Asn Tyr Asn Glu Met Ile Lys Asp
                85                  90                  95
Ile Glu Lys Gln Lys Lys Ser Cys Lys Glu Gln Thr Trp Lys Phe Leu
            100                 105                 110
Val Asn Glu Phe Lys Ser Asp Ile Gln Glu Tyr Asn Lys Lys Tyr Cys
        115                 120                 125
Gly Leu Glu Lys Gly Ile Asn Asn Leu Glu Lys Ala Ile Ser Glu Asn
    130                 135                 140
Gln Glu Glu Val Lys Lys Leu Glu Asn Glu
145                 150
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  1               5                  10                  15
ttg caa gtg tta gaa tgt gaa aat tgt tca atg act tat tat gat aga    96
Leu Gln Val Leu Glu Cys Glu Asn Cys Ser Met Thr Tyr Tyr Asp Arg
            20                  25                  30
gat tat aat aga gaa tgt gag att tgc cct tat tgc gat gct aaa aaa   144
Asp Tyr Asn Arg Glu Cys Glu Ile Cys Pro Tyr Cys Asp Ala Lys Lys
        35                  40                  45
cct gtc aga ctt gta gca aca agt tat tac caa aag agc gaa gtt ttt   192
Pro Val Arg Leu Val Ala Thr Ser Tyr Tyr Gln Lys Ser Glu Val Phe
    50                  55                  60
tat ttt gtc tcg aat ttt aca gac cct att ttt tta ccg aca acc tta   240
Tyr Phe Val Ser Asn Phe Thr Asp Pro Ile Phe Leu Pro Thr Thr Leu
65                  70                  75                  80
ttt aag ggg att gaa gtg gtt aaa agc gaa tgg gag ttt gca gag att   288
Phe Lys Gly Ile Glu Val Val Lys Ser Glu Trp Glu Phe Ala Glu Ile
```

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                85                  90                  95
gct aat aat ata ttg att ttt cat cat gac ata caa caa gaa aag att   336
Ala Asn Asn Ile Leu Ile Phe His His Asp Ile Gln Gln Glu Lys Ile
            100                 105                 110
ctc att aat aat aaa aga ttg gat cac tat agg ata gaa ata gat tta   384
Leu Ile Asn Asn Lys Arg Leu Asp His Tyr Arg Ile Glu Ile Asp Leu
        115                 120                 125
gaa aaa gaa ttg act att tca tac aat ggt ttt tta att aag gtt caa   432
Glu Lys Glu Leu Thr Ile Ser Tyr Asn Gly Phe Leu Ile Lys Val Gln
    130                 135                 140
aaa tgc                                                          438
Lys Cys
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            20                  25                  30
Asp Tyr Asn Arg Glu Cys Glu Ile Cys Pro Tyr Cys Asp Ala Lys Lys
        35                  40                  45
Pro Val Arg Leu Val Ala Thr Ser Tyr Tyr Gln Lys Ser Glu Val Phe
    50                  55                  60
Tyr Phe Val Ser Asn Phe Thr Asp Pro Ile Phe Leu Pro Thr Thr Leu
65                  70                  75                  80
Phe Lys Gly Ile Glu Val Val Lys Ser Glu Trp Glu Phe Ala Glu Ile
                85                  90                  95
Ala Asn Asn Ile Leu Ile Phe His His Asp Ile Gln Gln Glu Lys Ile
            100                 105                 110
Leu Ile Asn Asn Lys Arg Leu Asp His Tyr Arg Ile Glu Ile Asp Leu
        115                 120                 125
Glu Lys Glu Leu Thr Ile Ser Tyr Asn Gly Phe Leu Ile Lys Val Gln
    130                 135                 140
Lys Cys
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  1               5                  10                  15
acg ctt ttt gtg atc ggg ttt atg agc tgc tcg gca agg ctg cct att    96
Thr Leu Phe Val Ile Gly Phe Met Ser Cys Ser Ala Arg Leu Pro Ile
            20                  25                  30
tat gtg ctg ttt gta ggc tcg ttt ttc cct tct tca agt gct ggg ttt   144
Tyr Val Leu Phe Val Gly Ser Phe Phe Pro Ser Ser Ser Ala Gly Phe
        35                  40                  45
gtg ctg ttt tgc att tat att ttg ggg gcg gtt gtg gcg tta gtg atg   192
Val Leu Phe Cys Ile Tyr Ile Leu Gly Ala Val Val Ala Leu Val Met
    50                  55                  60
gcc aaa tta ctc aaa tta agc gtg ttt aaa gga caa acc gaa tct ttt   240
Ala Lys Leu Leu Lys Leu Ser Val Phe Lys Gly Gln Thr Glu Ser Phe
65                  70                  75                  80
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atc atg gaa atg ccc aaa tac cgc ttt ccc agt tgg aga atg gtc tat   288
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ttc agt atc tac acc aaa tcg ctt tct tac ctt aaa aag gct ggg act   336
Phe Ser Ile Tyr Thr Lys Ser Leu Ser Tyr Leu Lys Lys Ala Gly Thr
            100                 105                 110
tac att tta gtg gga gcg att tta atc tgg ttt atg tct caa tac cct   384
Tyr Ile Leu Val Gly Ala Ile Leu Ile Trp Phe Met Ser Gln Tyr Pro
        115                 120                 125
aaa agc gat gcg gcc atg aaa gct tat aaa caa gaa agc ttg tta gtg   432
Lys Ser Asp Ala Ala Met Lys Ala Tyr Lys Gln Glu Ser Leu Leu Val
    130                 135                 140
aat aag gat acc act ctt tca agc gaa gct aaa gaa gaa aaa tta aaa   480
Asn Lys Asp Thr Thr Leu Ser Ser Glu Ala Lys Glu Glu Lys Leu Lys
145                 150                 155                 160
gaa tta aaa aca gaa ttg gat aaa aag aat tta aaa aat agc att gta   528
Glu Leu Lys Thr Glu Leu Asp Lys Lys Asn Leu Lys Asn Ser Ile Val
                165                 170                 175
gga aga ggc ggg gcg tat tta gaa aaa gtc ttt agc cct atg gat ttt   576
Gly Arg Gly Gly Ala Tyr Leu Glu Lys Val Phe Ser Pro Met Asp Phe
            180                 185                 190
gat tgg cgt ttg agt gtg tcg ctt gta acc gga ttt atg gct aaa gag   624
Asp Trp Arg Leu Ser Val Ser Leu Val Thr Gly Phe Met Ala Lys Glu
        195                 200                 205
gtg gtg gtt tct act ttg ggc gtg ttg ttt tct tta ggg gat caa aat   672
Val Val Val Ser Thr Leu Gly Val Leu Phe Ser Leu Gly Asp Gln Asn
    210                 215                 220
gaa aaa tct gac gct ttt aga ggg att tta aga aaa gaa gtc agc gtg   720
Glu Lys Ser Asp Ala Phe Arg Gly Ile Leu Arg Lys Glu Val Ser Val
225                 230                 235                 240
cct agc gga atc gct ttt atc gtg ttt gtg atg ttt tat atc cct tgt   768
Pro Ser Gly Ile Ala Phe Ile Val Phe Val Met Phe Tyr Ile Pro Cys
                245                 250                 255
ttt gca gcg acc att act ttt ggt agg gaa gcg gga ggg ata aag ttt   816
Phe Ala Ala Thr Ile Thr Phe Gly Arg Glu Ala Gly Gly Ile Lys Phe
            260                 265                 270
gta gcg tat tta ttc atc ttc aca acc gtt gta gcg tat gcg ttt tcc   864
Val Ala Tyr Leu Phe Ile Phe Thr Thr Val Val Ala Tyr Ala Phe Ser
        275                 280                 285
ttg ata gct ttt tat gcg act caa att ttg gtt                      897
Leu Ile Ala Phe Tyr Ala Thr Gln Ile Leu Val
    290                 295
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            20                  25                  30
Tyr Val Leu Phe Val Gly Ser Phe Phe Pro Ser Ser Ser Ala Gly Phe
        35                  40                  45
Val Leu Phe Cys Ile Tyr Ile Leu Gly Ala Val Val Ala Leu Val Met
    50                  55                  60
Ala Lys Leu Leu Lys Leu Ser Val Phe Lys Gly Gln Thr Glu Ser Phe
65                  70                  75                  80
Ile Met Glu Met Pro Lys Tyr Arg Phe Pro Ser Trp Arg Met Val Tyr
                85                  90                  95
Phe Ser Ile Tyr Thr Lys Ser Leu Ser Tyr Leu Lys Lys Ala Gly Thr
            100                 105                 110
```

```
Tyr Ile Leu Val Gly Ala Ile Leu Ile Trp Phe Met Ser Gln Tyr Pro
        115                 120                 125
Lys Ser Asp Ala Ala Met Lys Ala Tyr Lys Gln Glu Ser Leu Leu Val
    130                 135                 140
Asn Lys Asp Thr Thr Leu Ser Ser Glu Ala Lys Glu Glu Lys Leu Lys
145                 150                 155                 160
Glu Leu Lys Thr Glu Leu Asp Lys Lys Asn Leu Lys Asn Ser Ile Val
                165                 170                 175
Gly Arg Gly Gly Ala Tyr Leu Glu Lys Val Phe Ser Pro Met Asp Phe
            180                 185                 190
Asp Trp Arg Leu Ser Val Ser Leu Val Thr Gly Phe Met Ala Lys Glu
        195                 200                 205
Val Val Val Ser Thr Leu Gly Val Leu Phe Ser Leu Gly Asp Gln Asn
    210                 215                 220
Glu Lys Ser Asp Ala Phe Arg Gly Ile Leu Arg Lys Glu Val Ser Val
225                 230                 235                 240
Pro Ser Gly Ile Ala Phe Ile Val Phe Val Met Phe Tyr Ile Pro Cys
                245                 250                 255
Phe Ala Ala Thr Ile Thr Phe Gly Arg Glu Ala Gly Gly Ile Lys Phe
            260                 265                 270
Val Ala Tyr Leu Phe Ile Phe Thr Thr Val Val Ala Tyr Ala Phe Ser
        275                 280                 285
Leu Ile Ala Phe Tyr Ala Thr Gln Ile Leu Val
    290                 295
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  1               5                  10                  15
gaa gct tgc gcg aaa aac ttt gga gcg ttt tgt gtg ttt gtg ggg att   96
Glu Ala Cys Ala Lys Asn Phe Gly Ala Phe Cys Val Phe Val Gly Ile
             20                  25                  30
gtg aga aaa gag gat aac att caa ggc ttg agt ttt gat att tat gaa   144
Val Arg Lys Glu Asp Asn Ile Gln Gly Leu Ser Phe Asp Ile Tyr Glu
         35                  40                  45
gcg cta tta aag act tgg ttt gaa aaa tgg cac cat aaa gcc aaa gat   192
Ala Leu Leu Lys Thr Trp Phe Glu Lys Trp His His Lys Ala Lys Asp
     50                  55                  60
ttg ggc gtg gtg tta aaa atg gcg cac agc ctg ggc gat gtt ttg ata   240
Leu Gly Val Val Leu Lys Met Ala His Ser Leu Gly Asp Val Leu Ile
 65                  70                  75                  80
gga caa agc tca ttt tta tgc gtt tca atg gga aag aat aga aaa aat   288
Gly Gln Ser Ser Phe Leu Cys Val Ser Met Gly Lys Asn Arg Lys Asn
                 85                  90                  95
gcc tta gaa cta tac gaa aat ttt att gaa gat ttt aag cat aac gct   336
Ala Leu Glu Leu Tyr Glu Asn Phe Ile Glu Asp Phe Lys His Asn Ala
            100                 105                 110
cct att tgg aaa tac gat tta atc cat aat aaa cgc att tat gct aaa   384
Pro Ile Trp Lys Tyr Asp Leu Ile His Asn Lys Arg Ile Tyr Ala Lys
        115                 120                 125
gaa aga agc cac cct tta aaa ggg agc ggg ctt tta gct               423
Glu Arg Ser His Pro Leu Lys Gly Ser Gly Leu Leu Ala
    130                 135                 140
<210> 14
<211> 141
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<212> PRT
<213> Helicobacter pylori
<400> 14
Ile Gln Gly Ala Leu Asp Thr Arg Glu Leu Leu Lys Ala Tyr Gln Glu
1 5 10 15
Glu Ala Cys Ala Lys Asn Phe Gly Ala Phe Cys Val Phe Val Gly Ile
20 25 30
Val Arg Lys Glu Asp Asn Ile Gln Gly Leu Ser Phe Asp Ile Tyr Glu
35 40 45
Ala Leu Leu Lys Thr Trp Phe Glu Lys Trp His His Lys Ala Lys Asp
50 55 60
Leu Gly Val Val Leu Lys Met Ala His Ser Leu Gly Asp Val Leu Ile
65 70 75 80
Gly Gln Ser Ser Phe Leu Cys Val Ser Met Gly Lys Asn Arg Lys Asn
85 90 95
Ala Leu Glu Leu Tyr Glu Asn Phe Ile Glu Asp Phe Lys His Asn Ala
100 105 110
Pro Ile Trp Lys Tyr Asp Leu Ile His Asn Lys Arg Ile Tyr Ala Lys
115 120 125
Glu Arg Ser His Pro Leu Lys Gly Ser Gly Leu Leu Ala
130 135 140
<210> 15
<211> 216
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(216)
<400> 15
gta gaa gtg cga ttt ttt gga ccc ata aaa gaa gaa aat ttt ttc atc 48
Val Glu Val Arg Phe Phe Gly Pro Ile Lys Glu Glu Asn Phe Phe Ile
1 5 10 15
aaa gcg aat gat ttg aag gaa tta aga gcg att tta caa gaa aaa gag 96
Lys Ala Asn Asp Leu Lys Glu Leu Arg Ala Ile Leu Gln Glu Lys Glu
20 25 30
ggc tta aaa gag tgg ttg ggc gtt tgc gcg ata gcc ctt aat gat cat 144
Gly Leu Lys Glu Trp Leu Gly Val Cys Ala Ile Ala Leu Asn Asp His
35 40 45
tta ata gac aat tta aac acg cct tta aaa gat ggc gat gta ata agt 192
Leu Ile Asp Asn Leu Asn Thr Pro Leu Lys Asp Gly Asp Val Ile Ser
50 55 60
ttg ttg cca ccg gtt tgt ggg ggc 216
Leu Leu Pro Pro Val Cys Gly Gly
65 70
<210> 16
<211> 72
<212> PRT
<213> Helicobacter pylori
<400> 16
Val Glu Val Arg Phe Phe Gly Pro Ile Lys Glu Glu Asn Phe Phe Ile
1 5 10 15
Lys Ala Asn Asp Leu Lys Glu Leu Arg Ala Ile Leu Gln Glu Lys Glu
20 25 30
Gly Leu Lys Glu Trp Leu Gly Val Cys Ala Ile Ala Leu Asn Asp His
35 40 45
Leu Ile Asp Asn Leu Asn Thr Pro Leu Lys Asp Gly Asp Val Ile Ser
50 55 60
Leu Leu Pro Pro Val Cys Gly Gly
65 70
<210> 17
<211> 156

<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(156)
<400> 17

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aac gag caa aaa cag caa ttg att gaa ggg gtt tca gat ttg atg gtt   48
Asn Glu Gln Lys Gln Gln Leu Ile Glu Gly Val Ser Asp Leu Met Val
  1               5                  10                  15
aag gtg ctg aat aaa aat aag gct tct att gtg gtc att ata gat gag   96
Lys Val Leu Asn Lys Asn Lys Ala Ser Ile Val Val Ile Ile Asp Glu
             20                  25                  30
gtc gat tct aat aat tat ggt ctt ggg ggc gag agc gtc cat cat ttg   144
Val Asp Ser Asn Asn Tyr Gly Leu Gly Gly Glu Ser Val His His Leu
         35                  40                  45
agg caa aaa aac                                                  156
Arg Gln Lys Asn
     50
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<210> 18
<211> 52
<212> PRT
<213> Helicobacter pylori
<400> 18

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Asn Glu Gln Lys Gln Gln Leu Ile Glu Gly Val Ser Asp Leu Met Val
  1               5                  10                  15
Lys Val Leu Asn Lys Asn Lys Ala Ser Ile Val Val Ile Ile Asp Glu
             20                  25                  30
Val Asp Ser Asn Asn Tyr Gly Leu Gly Gly Glu Ser Val His His Leu
         35                  40                  45
Arg Gln Lys Asn
     50
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<210> 19
<211> 600
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(600)
<400> 19

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att tat gcg cct att tta gcc ggg ctt gcc tct aat aac aaa tac tct   48
Ile Tyr Ala Pro Ile Leu Ala Gly Leu Ala Ser Asn Asn Lys Tyr Ser
  1               5                  10                  15
tta att ggc tcc gca aga gcg acg atc caa ctg ctc agc ttt gaa gtg   96
Leu Ile Gly Ser Ala Arg Ala Thr Ile Gln Leu Leu Ser Phe Glu Val
             20                  25                  30
gtc agc act tta acc att cta gcc ccc tta atg gtg gta gga tcg ctc   144
Val Ser Thr Leu Thr Ile Leu Ala Pro Leu Met Val Val Gly Ser Leu
         35                  40                  45
tct tta gtg gaa atc aat cat tac caa agc ggt ggg ttt tta gac tgg   192
Ser Leu Val Glu Ile Asn His Tyr Gln Ser Gly Gly Phe Leu Asp Trp
     50                  55                  60
ctt gtg ttt aag cag cct cta gcg ttt gtt ttg ttt ttg atc gca agt   240
Leu Val Phe Lys Gln Pro Leu Ala Phe Val Leu Phe Leu Ile Ala Ser
 65                  70                  75                  80
tat gcc gaa ttg aat cga acc ccc ttt gac ttg cta gag cat gaa gcc   288
Tyr Ala Glu Leu Asn Arg Thr Pro Phe Asp Leu Leu Glu His Glu Ala
                 85                  90                  95
gag atc gtg gcg ggg tat tgc acc gaa tac agc ggc ttg aaa tgg ggc   336
Glu Ile Val Ala Gly Tyr Cys Thr Glu Tyr Ser Gly Leu Lys Trp Gly
            100                 105                 110
atg ttc ttt tta gcg gaa tac gcg cat tta ttc gct ttt tct ttt gtg   384
```

```
Met Phe Phe Leu Ala Glu Tyr Ala His Leu Phe Ala Phe Ser Phe Val
        115                 120                 125
att tct att gtg ttt ttt ggc ggg ttt aac gca tgg ggc ttt atc cct   432
Ile Ser Ile Val Phe Phe Gly Gly Phe Asn Ala Trp Gly Phe Ile Pro
    130                 135                 140
gga ggc ata gcg att ttg att aaa gcg ggc ttt ttt gtc ttt tta tcc   480
Gly Gly Ile Ala Ile Leu Ile Lys Ala Gly Phe Phe Val Phe Leu Ser
145                 150                 155                 160
atg tgg gtt aga gcg act tat ccg cat gtg cgc cca gac caa ctg atg   528
Met Trp Val Arg Ala Thr Tyr Pro His Val Arg Pro Asp Gln Leu Met
                165                 170                 175
gat atg tgc tgg aaa atc atg ctg cct tta gcg tta ttg aac att gtg   576
Asp Met Cys Trp Lys Ile Met Leu Pro Leu Ala Leu Leu Asn Ile Val
            180                 185                 190
cta acg ggc att atc att tta att                                  600
Leu Thr Gly Ile Ile Ile Leu Ile
        195                 200
<210> 20
<211> 200
<212> PRT
<213> Helicobacter pylori
<400> 20
Ile Tyr Ala Pro Ile Leu Ala Gly Leu Ala Ser Asn Asn Lys Tyr Ser
  1               5                  10                  15
Leu Ile Gly Ser Ala Arg Ala Thr Ile Gln Leu Leu Ser Phe Glu Val
             20                  25                  30
Val Ser Thr Leu Thr Ile Leu Ala Pro Leu Met Val Val Gly Ser Leu
         35                  40                  45
Ser Leu Val Glu Ile Asn His Tyr Gln Ser Gly Gly Phe Leu Asp Trp
     50                  55                  60
Leu Val Phe Lys Gln Pro Leu Ala Phe Val Leu Phe Leu Ile Ala Ser
 65                  70                  75                  80
Tyr Ala Glu Leu Asn Arg Thr Pro Phe Asp Leu Leu Glu His Glu Ala
                 85                  90                  95
Glu Ile Val Ala Gly Tyr Cys Thr Glu Tyr Ser Gly Leu Lys Trp Gly
            100                 105                 110
Met Phe Phe Leu Ala Glu Tyr Ala His Leu Phe Ala Phe Ser Phe Val
        115                 120                 125
Ile Ser Ile Val Phe Phe Gly Gly Phe Asn Ala Trp Gly Phe Ile Pro
    130                 135                 140
Gly Gly Ile Ala Ile Leu Ile Lys Ala Gly Phe Phe Val Phe Leu Ser
145                 150                 155                 160
Met Trp Val Arg Ala Thr Tyr Pro His Val Arg Pro Asp Gln Leu Met
                165                 170                 175
Asp Met Cys Trp Lys Ile Met Leu Pro Leu Ala Leu Leu Asn Ile Val
            180                 185                 190
Leu Thr Gly Ile Ile Ile Leu Ile
        195                 200
<210> 21
<211> 474
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(474)
<400> 21
gac gcc aag gct caa gaa gtg gcg atg tgc gta gcg atg ggt aaa acc   48
Asp Ala Lys Ala Gln Glu Val Ala Met Cys Val Ala Met Gly Lys Thr
  1               5                  10                  15
cta aac gat aag ggg cgc ttg aaa cac tcc gtg cat gag ttt tac att   96
Leu Asn Asp Lys Gly Arg Leu Lys His Ser Val His Glu Phe Tyr Ile
```

```
          20                  25                  30
aaa tcc ccc gaa gaa atg gca aag ctc ttt gca gat att cca gaa gct   144
Lys Ser Pro Glu Glu Met Ala Lys Leu Phe Ala Asp Ile Pro Glu Ala
        35                  40                  45
tta gaa aac acc caa gaa atc gct gat aaa tgc gtt tta gag att gat   192
Leu Glu Asn Thr Gln Glu Ile Ala Asp Lys Cys Val Leu Glu Ile Asp
     50                  55                  60
tta aaa gac gat aaa aag aac ccc cca acc ccc cca agc ttc aaa ttc   240
Leu Lys Asp Asp Lys Lys Asn Pro Pro Thr Pro Pro Ser Phe Lys Phe
 65                  70                  75                  80
act aaa gct tac gct caa aat gag ggg ctg aat ttt gaa gat gac gct   288
Thr Lys Ala Tyr Ala Gln Asn Glu Gly Leu Asn Phe Glu Asp Asp Ala
                85                  90                  95
tct tat ttt gcc tat aag gct aga gaa ggc ttg aaa gag cgc tta gtt   336
Ser Tyr Phe Ala Tyr Lys Ala Arg Glu Gly Leu Lys Glu Arg Leu Val
            100                 105                 110
tta gta cca aaa gaa aag cat gat caa tat aaa gag cgc cta gaa aaa   384
Leu Val Pro Lys Glu Lys His Asp Gln Tyr Lys Glu Arg Leu Glu Lys
        115                 120                 125
gaa att gaa gtc att acg aac atg aaa ttc cca ggg tat atg ctg att   432
Glu Ile Glu Val Ile Thr Asn Met Lys Phe Pro Gly Tyr Met Leu Ile
    130                 135                 140
gtg tgg gat ttt atc cgt tat gct aag gaa atg ggc att cct           474
Val Trp Asp Phe Ile Arg Tyr Ala Lys Glu Met Gly Ile Pro
145                 150                 155
<210> 22
<211> 158
<212> PRT
<213> Helicobacter pylori
<400> 22
Asp Ala Lys Ala Gln Glu Val Ala Met Cys Val Ala Met Gly Lys Thr
  1               5                  10                  15
Leu Asn Asp Lys Gly Arg Leu Lys His Ser Val His Glu Phe Tyr Ile
            20                  25                  30
Lys Ser Pro Glu Glu Met Ala Lys Leu Phe Ala Asp Ile Pro Glu Ala
        35                  40                  45
Leu Glu Asn Thr Gln Glu Ile Ala Asp Lys Cys Val Leu Glu Ile Asp
    50                  55                  60
Leu Lys Asp Asp Lys Lys Asn Pro Pro Thr Pro Pro Ser Phe Lys Phe
 65                  70                  75                  80
Thr Lys Ala Tyr Ala Gln Asn Glu Gly Leu Asn Phe Glu Asp Asp Ala
                85                  90                  95
Ser Tyr Phe Ala Tyr Lys Ala Arg Glu Gly Leu Lys Glu Arg Leu Val
            100                 105                 110
Leu Val Pro Lys Glu Lys His Asp Gln Tyr Lys Glu Arg Leu Glu Lys
        115                 120                 125
Glu Ile Glu Val Ile Thr Asn Met Lys Phe Pro Gly Tyr Met Leu Ile
    130                 135                 140
Val Trp Asp Phe Ile Arg Tyr Ala Lys Glu Met Gly Ile Pro
145                 150                 155
<210> 23
<211> 512
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(510)
<400> 23
aag aat aaa gca ttc cac aac att gcc ctt gat att gaa acc cta aac    48
Lys Asn Lys Ala Phe His Asn Ile Ala Leu Asp Ile Glu Thr Leu Asn
  1               5                  10                  15
```

```
caa gaa gcc cta aaa aac act tat gat gtg agc gca atc agc ttt ggg   96
Gln Glu Ala Leu Lys Asn Thr Tyr Asp Val Ser Ala Ile Ser Phe Gly
             20                  25                  30
tta tac cct aaa att gcg aac gat tac gcc tta ctc ccc acg gca acg  144
Leu Tyr Pro Lys Ile Ala Asn Asp Tyr Ala Leu Leu Pro Thr Ala Thr
         35                  40                  45
agc ttt ggg aat ggc tat ggg cct aaa tta gtg aaa aaa aag ggc gtg  192
Ser Phe Gly Asn Gly Tyr Gly Pro Lys Leu Val Lys Lys Lys Gly Val
     50                  55                  60
aaa ttg aaa aaa gat ttt aga gtc gca tta agt ggg gag cac acc acc  240
Lys Leu Lys Lys Asp Phe Arg Val Ala Leu Ser Gly Glu His Thr Thr
 65                  70                  75                  80
aac gcc ctc ttg ttt aag atc tat tac aaa cat gcg cgc atc act tat  288
Asn Ala Leu Leu Phe Lys Ile Tyr Tyr Lys His Ala Arg Ile Thr Tyr
                 85                  90                  95
atg aat ttt tta gac att gaa aaa gcg gtt ttg gaa gaa aaa gtg cat  336
Met Asn Phe Leu Asp Ile Glu Lys Ala Val Leu Glu Glu Lys Val His
            100                 105                 110
gcg ggc gta ttg atc cat gag agt atc ttg gat ttt cat aat gaa tta  384
Ala Gly Val Leu Ile His Glu Ser Ile Leu Asp Phe His Asn Glu Leu
        115                 120                 125
gaa gtg gaa aaa gaa ttg tgg gat gtt tgg aaa gaa ctc att gaa gtg  432
Glu Val Glu Lys Glu Leu Trp Asp Val Trp Lys Glu Leu Ile Glu Val
    130                 135                 140
gat ttg ccc ttg cct tta ggg ggc atg gcg atc agg cga tct atc ccc  480
Asp Leu Pro Leu Pro Leu Gly Gly Met Ala Ile Arg Arg Ser Ile Pro
145                 150                 155                 160
ttg tat cgc gcg att ttg att aaa aag gct tt                       512
Leu Tyr Arg Ala Ile Leu Ile Lys Lys Ala
                165                 170
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<210> 24
<211> 170
<212> PRT
<213> Helicobacter pylori
<400> 24

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Lys Asn Lys Ala Phe His Asn Ile Ala Leu Asp Ile Glu Thr Leu Asn
  1               5                  10                  15
Gln Glu Ala Leu Lys Asn Thr Tyr Asp Val Ser Ala Ile Ser Phe Gly
             20                  25                  30
Leu Tyr Pro Lys Ile Ala Asn Asp Tyr Ala Leu Leu Pro Thr Ala Thr
         35                  40                  45
Ser Phe Gly Asn Gly Tyr Gly Pro Lys Leu Val Lys Lys Lys Gly Val
     50                  55                  60
Lys Leu Lys Lys Asp Phe Arg Val Ala Leu Ser Gly Glu His Thr Thr
 65                  70                  75                  80
Asn Ala Leu Leu Phe Lys Ile Tyr Tyr Lys His Ala Arg Ile Thr Tyr
                 85                  90                  95
Met Asn Phe Leu Asp Ile Glu Lys Ala Val Leu Glu Glu Lys Val His
            100                 105                 110
Ala Gly Val Leu Ile His Glu Ser Ile Leu Asp Phe His Asn Glu Leu
        115                 120                 125
Glu Val Glu Lys Glu Leu Trp Asp Val Trp Lys Glu Leu Ile Glu Val
    130                 135                 140
Asp Leu Pro Leu Pro Leu Gly Gly Met Ala Ile Arg Arg Ser Ile Pro
145                 150                 155                 160
Leu Tyr Arg Ala Ile Leu Ile Lys Lys Ala
                165                 170
```

<210> 25
<211> 432
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (1)..(432)
<400> 25
tta aaa atc att caa ggg gca tta gat act agg gag ctt tta aaa gcc 48
Leu Lys Ile Ile Gln Gly Ala Leu Asp Thr Arg Glu Leu Leu Lys Ala
1 5 10 15
tac caa gag gaa gct tgc gcg aaa aac ttt gga gcg ttt tgt gtg ttt 96
Tyr Gln Glu Glu Ala Cys Ala Lys Asn Phe Gly Ala Phe Cys Val Phe
20 25 30
gtg ggg att gtg aga aaa gag gat aac att caa ggc ttg agt ttt gat 144
Val Gly Ile Val Arg Lys Glu Asp Asn Ile Gln Gly Leu Ser Phe Asp
35 40 45
att tat gaa gcg cta tta aag act tgg ttt gaa aaa tgg cac cat aaa 192
Ile Tyr Glu Ala Leu Leu Lys Thr Trp Phe Glu Lys Trp His His Lys
50 55 60
gcc aaa gat ttg ggc gtg gtg tta aaa atg gcg cac agc ctg ggc gat 240
Ala Lys Asp Leu Gly Val Val Leu Lys Met Ala His Ser Leu Gly Asp
65 70 75 80
gtt ttg ata gga caa agc tca ttt tta tgc gtt tca atg gga aag aat 288
Val Leu Ile Gly Gln Ser Ser Phe Leu Cys Val Ser Met Gly Lys Asn
85 90 95
aga aaa aat gcc tta gaa cta tac gaa aat ttt att gaa gat ttt aag 336
Arg Lys Asn Ala Leu Glu Leu Tyr Glu Asn Phe Ile Glu Asp Phe Lys
100 105 110
cat aac gct cct att tgg aaa tac gat tta atc cat aat aaa cgc att 384
His Asn Ala Pro Ile Trp Lys Tyr Asp Leu Ile His Asn Lys Arg Ile
115 120 125
tat gct aaa gaa aga agc cac cct tta aaa ggg agc ggg ctt tta gct 432
Tyr Ala Lys Glu Arg Ser His Pro Leu Lys Gly Ser Gly Leu Leu Ala
130 135 140
<210> 26
<211> 144
<212> PRT
<213> Helicobacter pylori
<400> 26
Leu Lys Ile Ile Gln Gly Ala Leu Asp Thr Arg Glu Leu Leu Lys Ala
1 5 10 15
Tyr Gln Glu Glu Ala Cys Ala Lys Asn Phe Gly Ala Phe Cys Val Phe
20 25 30
Val Gly Ile Val Arg Lys Glu Asp Asn Ile Gln Gly Leu Ser Phe Asp
35 40 45
Ile Tyr Glu Ala Leu Leu Lys Thr Trp Phe Glu Lys Trp His His Lys
50 55 60
Ala Lys Asp Leu Gly Val Val Leu Lys Met Ala His Ser Leu Gly Asp
65 70 75 80
Val Leu Ile Gly Gln Ser Ser Phe Leu Cys Val Ser Met Gly Lys Asn
85 90 95
Arg Lys Asn Ala Leu Glu Leu Tyr Glu Asn Phe Ile Glu Asp Phe Lys
100 105 110
His Asn Ala Pro Ile Trp Lys Tyr Asp Leu Ile His Asn Lys Arg Ile
115 120 125
Tyr Ala Lys Glu Arg Ser His Pro Leu Lys Gly Ser Gly Leu Leu Ala
130 135 140
<210> 27
<211> 516
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(516)

<400> 27
tta agc ttt agc gcg gat aaa ttc ttt aac agt gcg caa gcg ggc att 48
Leu Ser Phe Ser Ala Asp Lys Phe Phe Asn Ser Ala Gln Ala Gly Ile
1 5 10 15
att atg ggg caa aaa gaa cgg gtt gaa gcg tta aaa aac cac ccc ctt 96
Ile Met Gly Gln Lys Glu Arg Val Glu Ala Leu Lys Asn His Pro Leu
20 25 30
tat aga gtt tta agg gtg ggt aaa atc acg ctc acc ttg ctt ttt tgc 144
Tyr Arg Val Leu Arg Val Gly Lys Ile Thr Leu Thr Leu Leu Phe Cys
35 40 45
agc cta aaa gca tgg ata aat cat caa gaa gac att aca atc cat gcg 192
Ser Leu Lys Ala Trp Ile Asn His Gln Glu Asp Ile Thr Ile His Ala
50 55 60
tta ttg aac caa act aaa gac gca tta ttg caa aaa gcc ctc aaa ctc 240
Leu Leu Asn Gln Thr Lys Asp Ala Leu Leu Gln Lys Ala Leu Lys Leu
65 70 75 80
tac gct ctt tta aag cct tta gaa ttg aat gtg agc ata gcc tct agc 288
Tyr Ala Leu Leu Lys Pro Leu Glu Leu Asn Val Ser Ile Ala Ser Ser
85 90 95
ttt tct aaa ata ggg aat ttg ttt ggt agg gaa tta gaa tcc ttt tgc 336
Phe Ser Lys Ile Gly Asn Leu Phe Gly Arg Glu Leu Glu Ser Phe Cys
100 105 110
gtg aaa atc cag ccc aaa aac acc cgt gct tta aat agt gag aaa ctt 384
Val Lys Ile Gln Pro Lys Asn Thr Arg Ala Leu Asn Ser Glu Lys Leu
115 120 125
tat tta aag ctt ttc caa aaa ggc gtt atc gca agg att tca tgc gaa 432
Tyr Leu Lys Leu Phe Gln Lys Gly Val Ile Ala Arg Ile Ser Cys Glu
130 135 140
ttc gtg tgc ttt gaa gtc ttt agc ttg aat gaa aaa gat ttt gaa aaa 480
Phe Val Cys Phe Glu Val Phe Ser Leu Asn Glu Lys Asp Phe Glu Lys
145 150 155 160
atc gct ctg gtt tta gaa gaa att ctt aat aaa gct 516
Ile Ala Leu Val Leu Glu Glu Ile Leu Asn Lys Ala
165 170

<210> 28
<211> 172
<212> PRT
<213> Helicobacter pylori
<400> 28
Leu Ser Phe Ser Ala Asp Lys Phe Phe Asn Ser Ala Gln Ala Gly Ile
1 5 10 15
Ile Met Gly Gln Lys Glu Arg Val Glu Ala Leu Lys Asn His Pro Leu
20 25 30
Tyr Arg Val Leu Arg Val Gly Lys Ile Thr Leu Thr Leu Leu Phe Cys
35 40 45
Ser Leu Lys Ala Trp Ile Asn His Gln Glu Asp Ile Thr Ile His Ala
50 55 60
Leu Leu Asn Gln Thr Lys Asp Ala Leu Leu Gln Lys Ala Leu Lys Leu
65 70 75 80
Tyr Ala Leu Leu Lys Pro Leu Glu Leu Asn Val Ser Ile Ala Ser Ser
85 90 95
Phe Ser Lys Ile Gly Asn Leu Phe Gly Arg Glu Leu Glu Ser Phe Cys
100 105 110
Val Lys Ile Gln Pro Lys Asn Thr Arg Ala Leu Asn Ser Glu Lys Leu
115 120 125
Tyr Leu Lys Leu Phe Gln Lys Gly Val Ile Ala Arg Ile Ser Cys Glu
130 135 140
Phe Val Cys Phe Glu Val Phe Ser Leu Asn Glu Lys Asp Phe Glu Lys
145 150 155 160
Ile Ala Leu Val Leu Glu Glu Ile Leu Asn Lys Ala
165 170

<210> 29
<211> 444
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(444)
<400> 29

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atc att act caa gct aga aag gct aat ggg gtg att gtt cta gcc tta   48
Ile Ile Thr Gln Ala Arg Lys Ala Asn Gly Val Ile Val Leu Ala Leu
  1               5                  10                  15

caa gac att aac caa cta agc gaa gtg aga aac gct caa agc ttt ata   96
Gln Asp Ile Asn Gln Leu Ser Glu Val Arg Asn Ala Gln Ser Phe Ile
             20                  25                  30

aaa aat atg ggg caa ttg att ttg tat ccc caa aga aat att gat acc  144
Lys Asn Met Gly Gln Leu Ile Leu Tyr Pro Gln Arg Asn Ile Asp Thr
         35                  40                  45

aaa gat tta aac gat aaa ttt ggc att aga cta agc gat aca gaa aaa  192
Lys Asp Leu Asn Asp Lys Phe Gly Ile Arg Leu Ser Asp Thr Glu Lys
     50                  55                  60

cat ttt tta gaa aac acc gcc gtt aat gaa tac aaa gtc tta ctc aaa  240
His Phe Leu Glu Asn Thr Ala Val Asn Glu Tyr Lys Val Leu Leu Lys
 65                  70                  75                  80

aac atg aat gat ggc tca tct aac att ata gat gtg agc cta agt tct  288
Asn Met Asn Asp Gly Ser Ser Asn Ile Ile Asp Val Ser Leu Ser Ser
                 85                  90                  95

ttg ggt aat tac cta caa atc ttt agc tct aat tct agc atg gta gaa  336
Leu Gly Asn Tyr Leu Gln Ile Phe Ser Ser Asn Ser Ser Met Val Glu
            100                 105                 110

cac att gat aat ctc att aag cat tac cct aaa act tgg cga gaa gtc  384
His Ile Asp Asn Leu Ile Lys His Tyr Pro Lys Thr Trp Arg Glu Val
        115                 120                 125

ttt gtg agt aac aaa cac gaa aat ttt gat gac aaa aaa cac tta gaa  432
Phe Val Ser Asn Lys His Glu Asn Phe Asp Asp Lys Lys His Leu Glu
    130                 135                 140

aag gtg ctt aaa                                                 444
Lys Val Leu Lys
145
```

<210> 30
<211> 148
<212> PRT
<213> Helicobacter pylori
<400> 30

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Ile Ile Thr Gln Ala Arg Lys Ala Asn Gly Val Ile Val Leu Ala Leu
  1               5                  10                  15
Gln Asp Ile Asn Gln Leu Ser Glu Val Arg Asn Ala Gln Ser Phe Ile
             20                  25                  30
Lys Asn Met Gly Gln Leu Ile Leu Tyr Pro Gln Arg Asn Ile Asp Thr
         35                  40                  45
Lys Asp Leu Asn Asp Lys Phe Gly Ile Arg Leu Ser Asp Thr Glu Lys
     50                  55                  60
His Phe Leu Glu Asn Thr Ala Val Asn Glu Tyr Lys Val Leu Leu Lys
 65                  70                  75                  80
Asn Met Asn Asp Gly Ser Ser Asn Ile Ile Asp Val Ser Leu Ser Ser
                 85                  90                  95
Leu Gly Asn Tyr Leu Gln Ile Phe Ser Ser Asn Ser Ser Met Val Glu
            100                 105                 110
His Ile Asp Asn Leu Ile Lys His Tyr Pro Lys Thr Trp Arg Glu Val
        115                 120                 125
Phe Val Ser Asn Lys His Glu Asn Phe Asp Asp Lys Lys His Leu Glu
    130                 135                 140
```

```
Lys Val Leu Lys
145
<210> 31
<211> 426
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(426)
<400> 31
acg gtg ggc gat gtt ttt ggt gaa aac ggg ctt tta aac gcg cta gat   48
Thr Val Gly Asp Val Phe Gly Glu Asn Gly Leu Leu Asn Ala Leu Asp
  1               5                  10                  15
cct acg gaa aga aaa aaa att gat caa atg ctt tta gag caa atc caa   96
Pro Thr Glu Arg Lys Lys Ile Asp Gln Met Leu Leu Glu Gln Ile Gln
             20                  25                  30
gcc cat tct tca ggg ttt gaa aaa ttc atc gtg aaa act tta ggg att   144
Ala His Ser Ser Gly Phe Glu Lys Phe Ile Val Lys Thr Leu Gly Ile
         35                  40                  45
gaa aat gta gag aat ttc atc aat aac tgg tat ggc aag caa agc ttg   192
Glu Asn Val Glu Asn Phe Ile Asn Asn Trp Tyr Gly Lys Gln Ser Leu
     50                  55                  60
agt tct ttt gcc aat aat ttt gtg cct gga ggc ttg aat caa gcc ctt   240
Ser Ser Phe Ala Asn Asn Phe Val Pro Gly Gly Leu Asn Gln Ala Leu
 65                  70                  75                  80
gat aaa ata ggc tct agc tct gat gcc aaa gac tta cag aac ttc ttg   288
Asp Lys Ile Gly Ser Ser Ser Asp Ala Lys Asp Leu Gln Asn Phe Leu
                 85                  90                  95
gat aaa acg act ttt ggg gat att tta aat caa atg att gaa caa gcc   336
Asp Lys Thr Thr Phe Gly Asp Ile Leu Asn Gln Met Ile Glu Gln Ala
            100                 105                 110
ccc tta atc aat aaa ctc att tct tgg ctg ggt ccg cag gat ttg agc   384
Pro Leu Ile Asn Lys Leu Ile Ser Trp Leu Gly Pro Gln Asp Leu Ser
        115                 120                 125
gtt tta gtg aat atc gct tta aat agc atc act aac cct agt           426
Val Leu Val Asn Ile Ala Leu Asn Ser Ile Thr Asn Pro Ser
    130                 135                 140
<210> 32
<211> 142
<212> PRT
<213> Helicobacter pylori
<400> 32
Thr Val Gly Asp Val Phe Gly Glu Asn Gly Leu Leu Asn Ala Leu Asp
  1               5                  10                  15
Pro Thr Glu Arg Lys Lys Ile Asp Gln Met Leu Leu Glu Gln Ile Gln
             20                  25                  30
Ala His Ser Ser Gly Phe Glu Lys Phe Ile Val Lys Thr Leu Gly Ile
         35                  40                  45
Glu Asn Val Glu Asn Phe Ile Asn Asn Trp Tyr Gly Lys Gln Ser Leu
     50                  55                  60
Ser Ser Phe Ala Asn Asn Phe Val Pro Gly Gly Leu Asn Gln Ala Leu
 65                  70                  75                  80
Asp Lys Ile Gly Ser Ser Ser Asp Ala Lys Asp Leu Gln Asn Phe Leu
                 85                  90                  95
Asp Lys Thr Thr Phe Gly Asp Ile Leu Asn Gln Met Ile Glu Gln Ala
            100                 105                 110
Pro Leu Ile Asn Lys Leu Ile Ser Trp Leu Gly Pro Gln Asp Leu Ser
        115                 120                 125
Val Leu Val Asn Ile Ala Leu Asn Ser Ile Thr Asn Pro Ser
    130                 135                 140
<210> 33
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<211> 357
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(357)
<400> 33
caa gcg cac cat ctt aaa aac ctt ttg gaa gcc ttt tat cac caa aat 48
Gln Ala His His Leu Lys Asn Leu Leu Glu Ala Phe Tyr His Gln Asn
1 5 10 15
aaa gag agt ttg ggc ttt ttt tcc cct tat ttt agt ttg cga tct caa 96
Lys Glu Ser Leu Gly Phe Phe Ser Pro Tyr Phe Ser Leu Arg Ser Gln
20 25 30
acc cct agc gtc tct tat gaa agc gcg tta gct tct tta gaa aac tat 144
Thr Pro Ser Val Ser Tyr Glu Ser Ala Leu Ala Ser Leu Glu Asn Tyr
35 40 45
ttt atg gct ttg ttc caa tcc cat ttt aaa gac gat acc gca ctc caa 192
Phe Met Ala Leu Phe Gln Ser His Phe Lys Asp Asp Thr Ala Leu Gln
50 55 60
cag aat ttt aaa gga ttg ttg caa gcc ttt gtt tct atg gct aaa gac 240
Gln Asn Phe Lys Gly Leu Leu Gln Ala Phe Val Ser Met Ala Lys Asp
65 70 75 80
aaa cga tcc caa atc gct ctt aac gcc caa gct aaa gac aac gcc aag 288
Lys Arg Ser Gln Ile Ala Leu Asn Ala Gln Ala Lys Asp Asn Ala Lys
85 90 95
cta act ttt aac gcc ttg tta gaa agc ctt agc gtg aat ttc ttt caa 336
Leu Thr Phe Asn Ala Leu Leu Glu Ser Leu Ser Val Asn Phe Phe Gln
100 105 110
tct tac aaa ata agc cat gag 357
Ser Tyr Lys Ile Ser His Glu
115
<210> 34
<211> 119
<212> PRT
<213> Helicobacter pylori
<400> 34
Gln Ala His His Leu Lys Asn Leu Leu Glu Ala Phe Tyr His Gln Asn
1 5 10 15
Lys Glu Ser Leu Gly Phe Phe Ser Pro Tyr Phe Ser Leu Arg Ser Gln
20 25 30
Thr Pro Ser Val Ser Tyr Glu Ser Ala Leu Ala Ser Leu Glu Asn Tyr
35 40 45
Phe Met Ala Leu Phe Gln Ser His Phe Lys Asp Asp Thr Ala Leu Gln
50 55 60
Gln Asn Phe Lys Gly Leu Leu Gln Ala Phe Val Ser Met Ala Lys Asp
65 70 75 80
Lys Arg Ser Gln Ile Ala Leu Asn Ala Gln Ala Lys Asp Asn Ala Lys
85 90 95
Leu Thr Phe Asn Ala Leu Leu Glu Ser Leu Ser Val Asn Phe Phe Gln
100 105 110
Ser Tyr Lys Ile Ser His Glu
115
<210> 35
<211> 980
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(978)
<400> 35
gtg ggt tct gga gcc ggg agg aaa gcc agc tct acg gtt tta act ttg 48

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Val Gly Ser Gly Ala Gly Arg Lys Ala Ser Ser Thr Val Leu Thr Leu
 1               5                  10                  15
caa gct tca gaa ggg att act agc agt aaa aat gcg gaa att tct ctt   96
Gln Ala Ser Glu Gly Ile Thr Ser Ser Lys Asn Ala Glu Ile Ser Leu
            20                  25                  30
tat gat ggc gcc acg ctc aat ttg gct tca aac agc gtt aaa tta atg   144
Tyr Asp Gly Ala Thr Leu Asn Leu Ala Ser Asn Ser Val Lys Leu Met
        35                  40                  45
ggt aat gtg tgg atg ggc cgt ttg caa tat gtg gga gcg tat ttg gcc   192
Gly Asn Val Trp Met Gly Arg Leu Gln Tyr Val Gly Ala Tyr Leu Ala
    50                  55                  60
cct tca tac agc acg ata aac act tca aaa gtg aca ggg gaa gtg aat   240
Pro Ser Tyr Ser Thr Ile Asn Thr Ser Lys Val Thr Gly Glu Val Asn
65                  70                  75                  80
ttt aac cat ctc act gtg ggc gat cac aac gcc gct caa gca ggc att   288
Phe Asn His Leu Thr Val Gly Asp His Asn Ala Ala Gln Ala Gly Ile
                85                  90                  95
atc gct agt aac aag act cat att ggc aca ctg gat ttg tgg caa agc   336
Ile Ala Ser Asn Lys Thr His Ile Gly Thr Leu Asp Leu Trp Gln Ser
            100                 105                 110
gcg gga cta aac att atc gcc cct cca gaa ggc ggt tat aag gat aaa   384
Ala Gly Leu Asn Ile Ile Ala Pro Pro Glu Gly Gly Tyr Lys Asp Lys
        115                 120                 125
cct aag gat aaa cct agt aac acc acg caa aat aat gct aac aac aac   432
Pro Lys Asp Lys Pro Ser Asn Thr Thr Gln Asn Asn Ala Asn Asn Asn
    130                 135                 140
caa caa aac agc gct caa aac aat agt aac act cag gtt att aac cca   480
Gln Gln Asn Ser Ala Gln Asn Asn Ser Asn Thr Gln Val Ile Asn Pro
145                 150                 155                 160
ccc aat agc gcg caa aaa aca gaa att caa ccc acg caa gtc att gat   528
Pro Asn Ser Ala Gln Lys Thr Glu Ile Gln Pro Thr Gln Val Ile Asp
                165                 170                 175
ggg cct ttt gct ggt ggc aaa gac acg gtt gtc aat att gat cgc atc   576
Gly Pro Phe Ala Gly Gly Lys Asp Thr Val Val Asn Ile Asp Arg Ile
            180                 185                 190
aac act aac gct gat ggc acg att aaa gtg gga ggg tat aaa gct tct   624
Asn Thr Asn Ala Asp Gly Thr Ile Lys Val Gly Gly Tyr Lys Ala Ser
        195                 200                 205
ctt acc acc aat gcg gct cat ttg cat atc ggc aaa ggc ggt atc aat   672
Leu Thr Thr Asn Ala Ala His Leu His Ile Gly Lys Gly Gly Ile Asn
    210                 215                 220
ctg tcc aat caa gcg agc ggg cgc acc ctt tta gtg gaa aat cta acc   720
Leu Ser Asn Gln Ala Ser Gly Arg Thr Leu Leu Val Glu Asn Leu Thr
225                 230                 235                 240
ggg aat atc acc gtt gat ggg cct tta aga gtg aat aat caa gtg ggt   768
Gly Asn Ile Thr Val Asp Gly Pro Leu Arg Val Asn Asn Gln Val Gly
                245                 250                 255
ggt tat gct ttg gca gga tca agc gcg aat ttt gag ttt aag gct ggt   816
Gly Tyr Ala Leu Ala Gly Ser Ser Ala Asn Phe Glu Phe Lys Ala Gly
            260                 265                 270
acg gat acc aaa aac ggc aca gcc act ttt aat aac gat att agt ttg   864
Thr Asp Thr Lys Asn Gly Thr Ala Thr Phe Asn Asn Asp Ile Ser Leu
        275                 280                 285
gga aga ttt gtg aat tta aaa gtg gat gct cat aca gct aat ttt aaa   912
Gly Arg Phe Val Asn Leu Lys Val Asp Ala His Thr Ala Asn Phe Lys
    290                 295                 300
ggt att gat act ggt aat ggt ggt ttc aac acc tta gat ttt agt ggc   960
Gly Ile Asp Thr Gly Asn Gly Gly Phe Asn Thr Leu Asp Phe Ser Gly
305                 310                 315                 320
gtt aca ggt aag gtc aat at                                       980
Val Thr Gly Lys Val Asn
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325

<210> 36
<211> 326
<212> PRT
<213> Helicobacter pylori
<400> 36

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Val Gly Ser Gly Ala Gly Arg Lys Ala Ser Ser Thr Val Leu Thr Leu
 1               5                  10                  15
Gln Ala Ser Glu Gly Ile Thr Ser Ser Lys Asn Ala Glu Ile Ser Leu
            20                  25                  30
Tyr Asp Gly Ala Thr Leu Asn Leu Ala Ser Asn Ser Val Lys Leu Met
        35                  40                  45
Gly Asn Val Trp Met Gly Arg Leu Gln Tyr Val Gly Ala Tyr Leu Ala
    50                  55                  60
Pro Ser Tyr Ser Thr Ile Asn Thr Ser Lys Val Thr Gly Glu Val Asn
65                  70                  75                  80
Phe Asn His Leu Thr Val Gly Asp His Asn Ala Ala Gln Ala Gly Ile
                85                  90                  95
Ile Ala Ser Asn Lys Thr His Ile Gly Thr Leu Asp Leu Trp Gln Ser
            100                 105                 110
Ala Gly Leu Asn Ile Ile Ala Pro Pro Glu Gly Gly Tyr Lys Asp Lys
        115                 120                 125
Pro Lys Asp Lys Pro Ser Asn Thr Thr Gln Asn Asn Ala Asn Asn Asn
    130                 135                 140
Gln Gln Asn Ser Ala Gln Asn Asn Ser Asn Thr Gln Val Ile Asn Pro
145                 150                 155                 160
Pro Asn Ser Ala Gln Lys Thr Glu Ile Gln Pro Thr Gln Val Ile Asp
                165                 170                 175
Gly Pro Phe Ala Gly Gly Lys Asp Thr Val Val Asn Ile Asp Arg Ile
            180                 185                 190
Asn Thr Asn Ala Asp Gly Thr Ile Lys Val Gly Gly Tyr Lys Ala Ser
        195                 200                 205
Leu Thr Thr Asn Ala Ala His Leu His Ile Gly Lys Gly Gly Ile Asn
    210                 215                 220
Leu Ser Asn Gln Ala Ser Gly Arg Thr Leu Leu Val Glu Asn Leu Thr
225                 230                 235                 240
Gly Asn Ile Thr Val Asp Gly Pro Leu Arg Val Asn Asn Gln Val Gly
                245                 250                 255
Gly Tyr Ala Leu Ala Gly Ser Ser Ala Asn Phe Glu Phe Lys Ala Gly
            260                 265                 270
Thr Asp Thr Lys Asn Gly Thr Ala Thr Phe Asn Asn Asp Ile Ser Leu
        275                 280                 285
Gly Arg Phe Val Asn Leu Lys Val Asp Ala His Thr Ala Asn Phe Lys
    290                 295                 300
Gly Ile Asp Thr Gly Asn Gly Gly Phe Asn Thr Leu Asp Phe Ser Gly
305                 310                 315                 320
Val Thr Gly Lys Val Asn
                325
```

<210> 37
<211> 362
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(360)
<400> 37

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agt aat tta tgt ggt aat ggt agt agc ggt agt agt ggc act act tgc   48
Ser Asn Leu Cys Gly Asn Gly Ser Ser Gly Ser Ser Gly Thr Thr Cys
 1               5                  10                  15
tcc ggt tgg ctt atc aac ctt tta ggg gca atc ccc acc aat gga gtg   96
Ser Gly Trp Leu Ile Asn Leu Leu Gly Ala Ile Pro Thr Asn Gly Val
```

```
          20                  25                  30
agc gat acg aat aat tta att aat ctg ctc act gaa ttc att aaa acc   144
Ser Asp Thr Asn Asn Leu Ile Asn Leu Leu Thr Glu Phe Ile Lys Thr
         35                  40                  45
gcc ggg ttt atc caa aat aat gat agt agt gta tct act agt ctt aca   192
Ala Gly Phe Ile Gln Asn Asn Asp Ser Ser Val Ser Thr Ser Leu Thr
     50                  55                  60
agc gct ttt caa gcc att acg agc gct att tct caa ggg ttt caa gcc   240
Ser Ala Phe Gln Ala Ile Thr Ser Ala Ile Ser Gln Gly Phe Gln Ala
 65                  70                  75                  80
tta caa aac gat att agc cct aat gcg att tta acc ttg ctc caa gag   288
Leu Gln Asn Asp Ile Ser Pro Asn Ala Ile Leu Thr Leu Leu Gln Glu
                85                  90                  95
att act tct aac acc acc acc att cag tca ttc tcg caa acc tta cgg   336
Ile Thr Ser Asn Thr Thr Thr Ile Gln Ser Phe Ser Gln Thr Leu Arg
            100                 105                 110
cag ctt tta ggg gat aaa aca ttc tt                                362
Gln Leu Leu Gly Asp Lys Thr Phe
        115                 120
<210> 38
<211> 120
<212> PRT
<213> Helicobacter pylori
<400> 38
Ser Asn Leu Cys Gly Asn Gly Ser Ser Gly Ser Ser Gly Thr Thr Cys
  1               5                  10                  15
Ser Gly Trp Leu Ile Asn Leu Leu Gly Ala Ile Pro Thr Asn Gly Val
             20                  25                  30
Ser Asp Thr Asn Asn Leu Ile Asn Leu Leu Thr Glu Phe Ile Lys Thr
         35                  40                  45
Ala Gly Phe Ile Gln Asn Asn Asp Ser Ser Val Ser Thr Ser Leu Thr
     50                  55                  60
Ser Ala Phe Gln Ala Ile Thr Ser Ala Ile Ser Gln Gly Phe Gln Ala
 65                  70                  75                  80
Leu Gln Asn Asp Ile Ser Pro Asn Ala Ile Leu Thr Leu Leu Gln Glu
                85                  90                  95
Ile Thr Ser Asn Thr Thr Thr Ile Gln Ser Phe Ser Gln Thr Leu Arg
            100                 105                 110
Gln Leu Leu Gly Asp Lys Thr Phe
        115                 120
<210> 39
<211> 448
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(447)
<400> 39
ctc ttt gca gat att cca gaa gct tta gaa aac acc caa gaa atc gct    48
Leu Phe Ala Asp Ile Pro Glu Ala Leu Glu Asn Thr Gln Glu Ile Ala
  1               5                  10                  15
gat aaa tgc gtt tta gag att gat tta aaa gac gat aaa aag aac ccc    96
Asp Lys Cys Val Leu Glu Ile Asp Leu Lys Asp Asp Lys Lys Asn Pro
             20                  25                  30
cca acc ccc cca agc ttc aaa ttc act aaa gct tac gct caa aat gag   144
Pro Thr Pro Pro Ser Phe Lys Phe Thr Lys Ala Tyr Ala Gln Asn Glu
         35                  40                  45
ggg ctg aat ttt gaa gat gac gct tct tat ttt gcc tat aag gct aga   192
Gly Leu Asn Phe Glu Asp Asp Ala Ser Tyr Phe Ala Tyr Lys Ala Arg
     50                  55                  60
gaa ggc ttg aaa gag cgc tta gtt tta gta cca aaa gaa aag cat gat   240
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```
Glu Gly Leu Lys Glu Arg Leu Val Leu Val Pro Lys Glu Lys His Asp
 65                  70                  75                  80
caa tat aaa gag cgc cta gaa aaa gaa att gaa gtc att acg aac atg   288
Gln Tyr Lys Glu Arg Leu Glu Lys Glu Ile Glu Val Ile Thr Asn Met
                 85                  90                  95
aaa ttc cca ggg tat atg ctg att gtg tgg gat ttt atc cgt tat gct   336
Lys Phe Pro Gly Tyr Met Leu Ile Val Trp Asp Phe Ile Arg Tyr Ala
            100                 105                 110
aag gaa atg ggc att cct gta ggg cct ggt agg ggg agt gcg gcc ggg   384
Lys Glu Met Gly Ile Pro Val Gly Pro Gly Arg Gly Ser Ala Ala Gly
        115                 120                 125
agc ttg gtg gct ttt gct tta aaa atc acg gat att gac cct ttg aaa   432
Ser Leu Val Ala Phe Ala Leu Lys Ile Thr Asp Ile Asp Pro Leu Lys
    130                 135                 140
tac gat ttg ctc ttt g                                           448
Tyr Asp Leu Leu Phe
145
<210> 40
<211> 149
<212> PRT
<213> Helicobacter pylori
<400> 40
Leu Phe Ala Asp Ile Pro Glu Ala Leu Glu Asn Thr Gln Glu Ile Ala
  1               5                  10                  15
Asp Lys Cys Val Leu Glu Ile Asp Leu Lys Asp Asp Lys Lys Asn Pro
             20                  25                  30
Pro Thr Pro Pro Ser Phe Lys Phe Thr Lys Ala Tyr Ala Gln Asn Glu
         35                  40                  45
Gly Leu Asn Phe Glu Asp Asp Ala Ser Tyr Phe Ala Tyr Lys Ala Arg
     50                  55                  60
Glu Gly Leu Lys Glu Arg Leu Val Leu Val Pro Lys Glu Lys His Asp
 65                  70                  75                  80
Gln Tyr Lys Glu Arg Leu Glu Lys Glu Ile Glu Val Ile Thr Asn Met
                 85                  90                  95
Lys Phe Pro Gly Tyr Met Leu Ile Val Trp Asp Phe Ile Arg Tyr Ala
            100                 105                 110
Lys Glu Met Gly Ile Pro Val Gly Pro Gly Arg Gly Ser Ala Ala Gly
        115                 120                 125
Ser Leu Val Ala Phe Ala Leu Lys Ile Thr Asp Ile Asp Pro Leu Lys
    130                 135                 140
Tyr Asp Leu Leu Phe
145
<210> 41
<211> 147
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(147)
<400> 41
caa tac gac ttt aag gcg atg ttt act ccc ttg atc atg caa gcg cag   48
Gln Tyr Asp Phe Lys Ala Met Phe Thr Pro Leu Ile Met Gln Ala Gln
  1               5                  10                  15
ttg agc tta aga aac att gat aat ttt gtg gaa aaa ggc tct gct ttg   96
Leu Ser Leu Arg Asn Ile Asp Asn Phe Val Glu Lys Gly Ser Ala Leu
             20                  25                  30
ata gat aaa ttt gac gct aac ccc tat aaa acg att ttt gga gaa agg   144
Ile Asp Lys Phe Asp Ala Asn Pro Tyr Lys Thr Ile Phe Gly Glu Arg
         35                  40                  45
aaa                                                             147
Lys
```

<210> 42
<211> 49
<212> PRT
<213> Helicobacter pylori
<400> 42
Gln Tyr Asp Phe Lys Ala Met Phe Thr Pro Leu Ile Met Gln Ala Gln
1 5 10 15
Leu Ser Leu Arg Asn Ile Asp Asn Phe Val Glu Lys Gly Ser Ala Leu
20 25 30
Ile Asp Lys Phe Asp Ala Asn Pro Tyr Lys Thr Ile Phe Gly Glu Arg
35 40 45
Lys

<210> 43
<211> 455
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(453)
<400> 43
aat ttc aat tca gcg aat att act acg agt ttg aat aat tcc tct atc 48
Asn Phe Asn Ser Ala Asn Ile Thr Thr Ser Leu Asn Asn Ser Ser Ile
1 5 10 15
gtg ttt aag ggg gcg gtc tct tta gga ggg cag ttt aat tta agc aat 96
Val Phe Lys Gly Ala Val Ser Leu Gly Gly Gln Phe Asn Leu Ser Asn
20 25 30
aac tct tct tta gat ttc caa ggc tct agc gct atc acc tct aac acg 144
Asn Ser Ser Leu Asp Phe Gln Gly Ser Ser Ala Ile Thr Ser Asn Thr
35 40 45
gcg ttt aat ttc tat gat aac gct ttt tct caa agc ccc atc act ttc 192
Ala Phe Asn Phe Tyr Asp Asn Ala Phe Ser Gln Ser Pro Ile Thr Phe
50 55 60
cat caa gcc ctt gac att aaa gcg ccc tta agt ttg gga ggc aac ctt 240
His Gln Ala Leu Asp Ile Lys Ala Pro Leu Ser Leu Gly Gly Asn Leu
65 70 75 80
tta aac cct aac aac agc agc gtg ctg gat tta aaa aac agc cag ctt 288
Leu Asn Pro Asn Asn Ser Ser Val Leu Asp Leu Lys Asn Ser Gln Leu
85 90 95
gtt ttt ggc gat caa ggg agt ttg aat atc gct aac att gat tta cta 336
Val Phe Gly Asp Gln Gly Ser Leu Asn Ile Ala Asn Ile Asp Leu Leu
100 105 110
agc gat cta aat gat aat aaa aat cgt gtg tat aac atc att caa gcg 384
Ser Asp Leu Asn Asp Asn Lys Asn Arg Val Tyr Asn Ile Ile Gln Ala
115 120 125
gac atg aat agt aat tgg tat gag cgt atc agc ttc ttt ggc atg cac 432
Asp Met Asn Ser Asn Trp Tyr Glu Arg Ile Ser Phe Phe Gly Met His
130 135 140
atc aat gac ggg att tat gat gc 455
Ile Asn Asp Gly Ile Tyr Asp
145 150
<210> 44
<211> 151
<212> PRT
<213> Helicobacter pylori
<400> 44
Asn Phe Asn Ser Ala Asn Ile Thr Thr Ser Leu Asn Asn Ser Ser Ile
1 5 10 15
Val Phe Lys Gly Ala Val Ser Leu Gly Gly Gln Phe Asn Leu Ser Asn
20 25 30
Asn Ser Ser Leu Asp Phe Gln Gly Ser Ser Ala Ile Thr Ser Asn Thr

```
        35                  40                  45
Ala Phe Asn Phe Tyr Asp Asn Ala Phe Ser Gln Ser Pro Ile Thr Phe
    50                  55                  60
His Gln Ala Leu Asp Ile Lys Ala Pro Leu Ser Leu Gly Gly Asn Leu
65                  70                  75                  80
Leu Asn Pro Asn Asn Ser Ser Val Leu Asp Leu Lys Asn Ser Gln Leu
                85                  90                  95
Val Phe Gly Asp Gln Gly Ser Leu Asn Ile Ala Asn Ile Asp Leu Leu
            100                 105                 110
Ser Asp Leu Asn Asp Asn Lys Asn Arg Val Tyr Asn Ile Ile Gln Ala
        115                 120                 125
Asp Met Asn Ser Asn Trp Tyr Glu Arg Ile Ser Phe Phe Gly Met His
    130                 135                 140
Ile Asn Asp Gly Ile Tyr Asp
145                 150
<210> 45
<211> 333
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(333)
<400> 45
gat ttt agt ttc aac gca caa ggc aat gtt ttt gtg caa aat tcc act   48
Asp Phe Ser Phe Asn Ala Gln Gly Asn Val Phe Val Gln Asn Ser Thr
  1               5                  10                  15
ttc tct aac gcc aat gga ggc acg ctc tct ttt aac gca gga aat tcg   96
Phe Ser Asn Ala Asn Gly Gly Thr Leu Ser Phe Asn Ala Gly Asn Ser
            20                  25                  30
ctc att ttt gcc gga aac aat cat att gca ttc act aac cac gct gga   144
Leu Ile Phe Ala Gly Asn Asn His Ile Ala Phe Thr Asn His Ala Gly
        35                  40                  45
act ctt caa tta ttg tcc gat caa gtt tct aac att aac atc acc acg   192
Thr Leu Gln Leu Leu Ser Asp Gln Val Ser Asn Ile Asn Ile Thr Thr
    50                  55                  60
ctt aac gct agc aac ggc ctt aag att aac gcc gct aat aac aat gtt   240
Leu Asn Ala Ser Asn Gly Leu Lys Ile Asn Ala Ala Asn Asn Asn Val
65                  70                  75                  80
tct gtg tct caa ggc aat ctg ttt gtc agc gct agc tgc gcg caa caa   288
Ser Val Ser Gln Gly Asn Leu Phe Val Ser Ala Ser Cys Ala Gln Gln
                85                  90                  95
agc gat cca act aca gct aat att gca aac cct tgc gcg ctt agc       333
Ser Asp Pro Thr Thr Ala Asn Ile Ala Asn Pro Cys Ala Leu Ser
            100                 105                 110
<210> 46
<211> 111
<212> PRT
<213> Helicobacter pylori
<400> 46
Asp Phe Ser Phe Asn Ala Gln Gly Asn Val Phe Val Gln Asn Ser Thr
  1               5                  10                  15
Phe Ser Asn Ala Asn Gly Gly Thr Leu Ser Phe Asn Ala Gly Asn Ser
            20                  25                  30
Leu Ile Phe Ala Gly Asn Asn His Ile Ala Phe Thr Asn His Ala Gly
        35                  40                  45
Thr Leu Gln Leu Leu Ser Asp Gln Val Ser Asn Ile Asn Ile Thr Thr
    50                  55                  60
Leu Asn Ala Ser Asn Gly Leu Lys Ile Asn Ala Ala Asn Asn Asn Val
65                  70                  75                  80
Ser Val Ser Gln Gly Asn Leu Phe Val Ser Ala Ser Cys Ala Gln Gln
                85                  90                  95
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Ser Asp Pro Thr Thr Ala Asn Ile Ala Asn Pro Cys Ala Leu Ser
            100                 105                 110
<210> 47
<211> 674
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(672)
<400> 47
ttg cgc ttg ggc caa ttc aat ggc aat tct ttc aca agc tat aag gat   48
Leu Arg Leu Gly Gln Phe Asn Gly Asn Ser Phe Thr Ser Tyr Lys Asp
  1               5                  10                  15
agc gct gat cgc acc acg aga gtg gat ttc aac gct aaa aat atc tta   96
Ser Ala Asp Arg Thr Thr Arg Val Asp Phe Asn Ala Lys Asn Ile Leu
             20                  25                  30
att gat aat ttt tta gaa atc aat aat cgt gtg ggt tct gga gcc ggg   144
Ile Asp Asn Phe Leu Glu Ile Asn Asn Arg Val Gly Ser Gly Ala Gly
         35                  40                  45
agg aaa gcc agc tct acg gtt tta act ttg caa gct tca gaa ggg att   192
Arg Lys Ala Ser Ser Thr Val Leu Thr Leu Gln Ala Ser Glu Gly Ile
     50                  55                  60
act agc agt aaa aat gcg gaa att tct ctt tat gat ggc gcc acg ctc   240
Thr Ser Ser Lys Asn Ala Glu Ile Ser Leu Tyr Asp Gly Ala Thr Leu
 65                  70                  75                  80
aat ttg gct tca aac agc gtt aaa tta atg ggt aat gtg tgg atg ggc   288
Asn Leu Ala Ser Asn Ser Val Lys Leu Met Gly Asn Val Trp Met Gly
                 85                  90                  95
cgt ttg caa tat gtg gga gcg tat ttg gcc cct tca tac agc acg ata   336
Arg Leu Gln Tyr Val Gly Ala Tyr Leu Ala Pro Ser Tyr Ser Thr Ile
            100                 105                 110
aac act tca aaa gtg aca ggg gaa gtg aat ttt aac cat ctc act gtg   384
Asn Thr Ser Lys Val Thr Gly Glu Val Asn Phe Asn His Leu Thr Val
        115                 120                 125
ggc gat cac aac gcc gct caa gca ggc att atc gct agt aac aag act   432
Gly Asp His Asn Ala Ala Gln Ala Gly Ile Ile Ala Ser Asn Lys Thr
    130                 135                 140
cat att ggc aca ctg gat ttg tgg caa agc gcg gga cta aac att atc   480
His Ile Gly Thr Leu Asp Leu Trp Gln Ser Ala Gly Leu Asn Ile Ile
145                 150                 155                 160
gcc cct cca gaa ggc ggt tat aag gat aaa cct aag gat aaa cct agt   528
Ala Pro Pro Glu Gly Gly Tyr Lys Asp Lys Pro Lys Asp Lys Pro Ser
                165                 170                 175
aac acc acg caa aat aat gct aac aac aac caa caa aac agc gct caa   576
Asn Thr Thr Gln Asn Asn Ala Asn Asn Asn Gln Gln Asn Ser Ala Gln
            180                 185                 190
aac aat agt aac act cag gtt att aac cca ccc aat agc gcg caa aaa   624
Asn Asn Ser Asn Thr Gln Val Ile Asn Pro Pro Asn Ser Ala Gln Lys
        195                 200                 205
aca gaa att caa ccc acg caa gtc att gat ggg cct ttt gct ggt ggc   672
Thr Glu Ile Gln Pro Thr Gln Val Ile Asp Gly Pro Phe Ala Gly Gly
    210                 215                 220
aa                                                               674
<210> 48
<211> 224
<212> PRT
<213> Helicobacter pylori
<400> 48
Leu Arg Leu Gly Gln Phe Asn Gly Asn Ser Phe Thr Ser Tyr Lys Asp
  1               5                  10                  15
Ser Ala Asp Arg Thr Thr Arg Val Asp Phe Asn Ala Lys Asn Ile Leu
```

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            20                  25                  30
Ile Asp Asn Phe Leu Glu Ile Asn Asn Arg Val Gly Ser Gly Ala Gly
        35                  40                  45
Arg Lys Ala Ser Ser Thr Val Leu Thr Leu Gln Ala Ser Glu Gly Ile
    50                  55                  60
Thr Ser Ser Lys Asn Ala Glu Ile Ser Leu Tyr Asp Gly Ala Thr Leu
65                  70                  75                  80
Asn Leu Ala Ser Asn Ser Val Lys Leu Met Gly Asn Val Trp Met Gly
                85                  90                  95
Arg Leu Gln Tyr Val Gly Ala Tyr Leu Ala Pro Ser Tyr Ser Thr Ile
            100                 105                 110
Asn Thr Ser Lys Val Thr Gly Glu Val Asn Phe Asn His Leu Thr Val
        115                 120                 125
Gly Asp His Asn Ala Ala Gln Ala Gly Ile Ile Ala Ser Asn Lys Thr
    130                 135                 140
His Ile Gly Thr Leu Asp Leu Trp Gln Ser Ala Gly Leu Asn Ile Ile
145                 150                 155                 160
Ala Pro Pro Glu Gly Gly Tyr Lys Asp Lys Pro Lys Asp Lys Pro Ser
                165                 170                 175
Asn Thr Thr Gln Asn Asn Ala Asn Asn Asn Gln Gln Asn Ser Ala Gln
            180                 185                 190
Asn Asn Ser Asn Thr Gln Val Ile Asn Pro Pro Asn Ser Ala Gln Lys
        195                 200                 205
Thr Glu Ile Gln Pro Thr Gln Val Ile Asp Gly Pro Phe Ala Gly Gly
    210                 215                 220
<210> 49
<211> 284
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(282)
<400> 49
aga ggc ttg cat gat ttt tgg caa aaa ggg tat ttt aac ttt tta agc   48
Arg Gly Leu His Asp Phe Trp Gln Lys Gly Tyr Phe Asn Phe Leu Ser
  1               5                  10                  15
aat ggc tat gtt ttt gtc aat aac agc tct ttt agc aac gct aca gga   96
Asn Gly Tyr Val Phe Val Asn Asn Ser Ser Phe Ser Asn Ala Thr Gly
            20                  25                  30
ggc agt ttg aat ttt gtc gcc aac aag tct att att ttt aat ggc gat  144
Gly Ser Leu Asn Phe Val Ala Asn Lys Ser Ile Ile Phe Asn Gly Asp
        35                  40                  45
aat acg att gac ttt agc aag tat cag ggc gca ttg att ttt gct tct  192
Asn Thr Ile Asp Phe Ser Lys Tyr Gln Gly Ala Leu Ile Phe Ala Ser
    50                  55                  60
aat gat gtt tct aat atc aat atc acc acc cta aac gct act aat ggc  240
Asn Asp Val Ser Asn Ile Asn Ile Thr Thr Leu Asn Ala Thr Asn Gly
65                  70                  75                  80
tta agc ctt aat gcg ggt ttg aat aac gtg agc gtt caa aaa gg        284
Leu Ser Leu Asn Ala Gly Leu Asn Asn Val Ser Val Gln Lys
                85                  90

<210> 50
<211> 94
<212> PRT
<213> Helicobacter pylori
<400> 50
Arg Gly Leu His Asp Phe Trp Gln Lys Gly Tyr Phe Asn Phe Leu Ser
  1               5                  10                  15
Asn Gly Tyr Val Phe Val Asn Asn Ser Ser Phe Ser Asn Ala Thr Gly
            20                  25                  30
Gly Ser Leu Asn Phe Val Ala Asn Lys Ser Ile Ile Phe Asn Gly Asp
```

```
        35                  40                  45
Asn Thr Ile Asp Phe Ser Lys Tyr Gln Gly Ala Leu Ile Phe Ala Ser
    50                  55                  60
Asn Asp Val Ser Asn Ile Asn Ile Thr Thr Leu Asn Ala Thr Asn Gly
65                  70                  75                  80
Leu Ser Leu Asn Ala Gly Leu Asn Asn Val Ser Val Gln Lys
                85                  90
```

<210> 51
<211> 498
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(498)
<400> 51

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aaa att tta gtg att caa ggg cct aat tta aac atg tta gga cac aga   48
Lys Ile Leu Val Ile Gln Gly Pro Asn Leu Asn Met Leu Gly His Arg
 1               5                  10                  15
gac cca agg ctt tat ggt atg gta acc tta gac caa atc cat gaa atc   96
Asp Pro Arg Leu Tyr Gly Met Val Thr Leu Asp Gln Ile His Glu Ile
            20                  25                  30
atg caa act ttc gtg aaa caa ggc aat tta gat gtg gaa tta gag ttt  144
Met Gln Thr Phe Val Lys Gln Gly Asn Leu Asp Val Glu Leu Glu Phe
        35                  40                  45
ttt caa act aat ttt gag ggc gaa atc att gat aaa atc caa gag agc  192
Phe Gln Thr Asn Phe Glu Gly Glu Ile Ile Asp Lys Ile Gln Glu Ser
    50                  55                  60
gtg ggc agc gat tat gaa ggg atc atc att aac cct gga gcg ttt tcg  240
Val Gly Ser Asp Tyr Glu Gly Ile Ile Ile Asn Pro Gly Ala Phe Ser
65                  70                  75                  80
cac act tct att gcg att gca gat gcg atc atg cta gcg ggc aaa ccc  288
His Thr Ser Ile Ala Ile Ala Asp Ala Ile Met Leu Ala Gly Lys Pro
                85                  90                  95
gtt att gaa gtg cat ctc act aac att caa gcc aga gag gaa ttc agg  336
Val Ile Glu Val His Leu Thr Asn Ile Gln Ala Arg Glu Glu Phe Arg
            100                 105                 110
aaa aat tct tac act gga gcg gct tgt gga ggc gtg atc atg gga ttt  384
Lys Asn Ser Tyr Thr Gly Ala Ala Cys Gly Gly Val Ile Met Gly Phe
        115                 120                 125
ggc ccg ctt ggc tac aac atg gct tta atg gcg atg gtc aat att tta  432
Gly Pro Leu Gly Tyr Asn Met Ala Leu Met Ala Met Val Asn Ile Leu
    130                 135                 140
gcc gaa atg aaa gcg ttc caa gaa gcc caa aaa aac aac cct aat aac  480
Ala Glu Met Lys Ala Phe Gln Glu Ala Gln Lys Asn Asn Pro Asn Asn
145                 150                 155                 160
ccc att aac aat caa aaa                                         498
Pro Ile Asn Asn Gln Lys
                165
```

<210> 52
<211> 166
<212> PRT
<213> Helicobacter pylori
<400> 52

```
Lys Ile Leu Val Ile Gln Gly Pro Asn Leu Asn Met Leu Gly His Arg
 1               5                  10                  15
Asp Pro Arg Leu Tyr Gly Met Val Thr Leu Asp Gln Ile His Glu Ile
            20                  25                  30
Met Gln Thr Phe Val Lys Gln Gly Asn Leu Asp Val Glu Leu Glu Phe
        35                  40                  45
Phe Gln Thr Asn Phe Glu Gly Glu Ile Ile Asp Lys Ile Gln Glu Ser
    50                  55                  60
```

```
Val Gly Ser Asp Tyr Glu Gly Ile Ile Ile Asn Pro Gly Ala Phe Ser
 65                  70                  75                  80
His Thr Ser Ile Ala Ile Ala Asp Ala Ile Met Leu Ala Gly Lys Pro
                 85                  90                  95
Val Ile Glu Val His Leu Thr Asn Ile Gln Ala Arg Glu Glu Phe Arg
            100                 105                 110
Lys Asn Ser Tyr Thr Gly Ala Ala Cys Gly Gly Val Ile Met Gly Phe
        115                 120                 125
Gly Pro Leu Gly Tyr Asn Met Ala Leu Met Ala Met Val Asn Ile Leu
    130                 135                 140
Ala Glu Met Lys Ala Phe Gln Glu Ala Gln Lys Asn Asn Pro Asn Asn
145                 150                 155                 160
Pro Ile Asn Asn Gln Lys
                165
```

<210> 53
<211> 75
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(75)
<400> 53

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caa tct ttg ata aca ata ata aat cgg cta atg caa aaa cag gac cag   48
Gln Ser Leu Ile Thr Ile Ile Asn Arg Leu Met Gln Lys Gln Asp Gln
  1               5                  10                  15
cga cta tca tcg ctc aag gca caa aaa                               75
Arg Leu Ser Ser Leu Lys Ala Gln Lys
            20                  25
```

<210> 54
<211> 25
<212> PRT
<213> Helicobacter pylori
<400> 54

```
Gln Ser Leu Ile Thr Ile Ile Asn Arg Leu Met Gln Lys Gln Asp Gln
  1               5                  10                  15
Arg Leu Ser Ser Leu Lys Ala Gln Lys
            20                  25
```

<210> 55
<211> 679
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(678)
<400> 55

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ttt aac aac agc gct tct ttt aat ttc aat aat tct aac gcg acc act   48
Phe Asn Asn Ser Ala Ser Phe Asn Phe Asn Asn Ser Asn Ala Thr Thr
  1               5                  10                  15
tcg ttt gtg ggg gat ttc act aac gct aat tca aat ttg caa atc gcc   96
Ser Phe Val Gly Asp Phe Thr Asn Ala Asn Ser Asn Leu Gln Ile Ala
            20                  25                  30
ggg aac gct gtt ttt ggg aac tct act aat ggc tct caa aat acc gct   144
Gly Asn Ala Val Phe Gly Asn Ser Thr Asn Gly Ser Gln Asn Thr Ala
        35                  40                  45
aat ttt aat aat acc ggc tct gtt aat att tca ggg aat gca acc ttt   192
Asn Phe Asn Asn Thr Gly Ser Val Asn Ile Ser Gly Asn Ala Thr Phe
    50                  55                  60
gat aat gtg gtg ttt aat ggc cct acg aac acg agc gtg aaa ggg cag   240
Asp Asn Val Val Phe Asn Gly Pro Thr Asn Thr Ser Val Lys Gly Gln
65                  70                  75                  80
gtt act tta aat aac atc act tta aaa aac ctg aac gcc cct ttg tct   288
```

```
Val Thr Leu Asn Asn Ile Thr Leu Lys Asn Leu Asn Ala Pro Leu Ser
                  85                  90                  95
ttt ggc gat ggg acg att act ttt aac gct cat tcg gtg att aat att   336
Phe Gly Asp Gly Thr Ile Thr Phe Asn Ala His Ser Val Ile Asn Ile
             100                 105                 110
gct gaa tct atc act aat ggc aac cct atc act ctt gta agc tct tct   384
Ala Glu Ser Ile Thr Asn Gly Asn Pro Ile Thr Leu Val Ser Ser Ser
         115                 120                 125
aaa gaa att gaa tac aac aac gct ttc agt aaa aat cta tgg cag ctc   432
Lys Glu Ile Glu Tyr Asn Asn Ala Phe Ser Lys Asn Leu Trp Gln Leu
     130                 135                 140
atc aac tac caa ggg cat ggg gca agc agt gaa aag ctc gtc tct agc   480
Ile Asn Tyr Gln Gly His Gly Ala Ser Ser Glu Lys Leu Val Ser Ser
145                 150                 155                 160
gcg ggt aat ggc gtt tat gat gtg gtg tat tct ttc aat aac caa acc   528
Ala Gly Asn Gly Val Tyr Asp Val Val Tyr Ser Phe Asn Asn Gln Thr
                 165                 170                 175
tac aat ttc caa gag gtt ttt tca caa aac agc att tct atc cgg cgt   576
Tyr Asn Phe Gln Glu Val Phe Ser Gln Asn Ser Ile Ser Ile Arg Arg
             180                 185                 190
ttg ggc gtt aac atg gtg ttt gat tat gtg gat atg gaa aaa tcg gat   624
Leu Gly Val Asn Met Val Phe Asp Tyr Val Asp Met Glu Lys Ser Asp
         195                 200                 205
cat tta tat tat caa aac gct ctc ggt ttt atg acc tac atg cct aat   672
His Leu Tyr Tyr Gln Asn Ala Leu Gly Phe Met Thr Tyr Met Pro Asn
     210                 215                 220
agc tat a                                                        679
Ser Tyr
225
<210> 56
<211> 226
<212> PRT
<213> Helicobacter pylori
<400> 56
Phe Asn Asn Ser Ala Ser Phe Asn Phe Asn Asn Ser Asn Ala Thr Thr
  1               5                  10                  15
Ser Phe Val Gly Asp Phe Thr Asn Ala Asn Ser Asn Leu Gln Ile Ala
             20                  25                  30
Gly Asn Ala Val Phe Gly Asn Ser Thr Asn Gly Ser Gln Asn Thr Ala
         35                  40                  45
Asn Phe Asn Asn Thr Gly Ser Val Asn Ile Ser Gly Asn Ala Thr Phe
     50                  55                  60
Asp Asn Val Val Phe Asn Gly Pro Thr Asn Thr Ser Val Lys Gly Gln
 65                  70                  75                  80
Val Thr Leu Asn Asn Ile Thr Leu Lys Asn Leu Asn Ala Pro Leu Ser
                 85                  90                  95
Phe Gly Asp Gly Thr Ile Thr Phe Asn Ala His Ser Val Ile Asn Ile
             100                 105                 110
Ala Glu Ser Ile Thr Asn Gly Asn Pro Ile Thr Leu Val Ser Ser Ser
         115                 120                 125
Lys Glu Ile Glu Tyr Asn Asn Ala Phe Ser Lys Asn Leu Trp Gln Leu
     130                 135                 140
Ile Asn Tyr Gln Gly His Gly Ala Ser Ser Glu Lys Leu Val Ser Ser
145                 150                 155                 160
Ala Gly Asn Gly Val Tyr Asp Val Val Tyr Ser Phe Asn Asn Gln Thr
                 165                 170                 175
Tyr Asn Phe Gln Glu Val Phe Ser Gln Asn Ser Ile Ser Ile Arg Arg
             180                 185                 190
Leu Gly Val Asn Met Val Phe Asp Tyr Val Asp Met Glu Lys Ser Asp
         195                 200                 205
His Leu Tyr Tyr Gln Asn Ala Leu Gly Phe Met Thr Tyr Met Pro Asn
```

```
   210                 215                 220
Ser Tyr
225
<210> 57
<211> 750
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(750)
<400> 57
aac gcc acg atc aac gat tat gcg agc ttg att gcg agt aat ggc tct   48
Asn Ala Thr Ile Asn Asp Tyr Ala Ser Leu Ile Ala Ser Asn Gly Ser
  1               5                  10                  15
cac ctt aat ttt aac ggg gcg gtt aat ttc aat tca gcg aat att act   96
His Leu Asn Phe Asn Gly Ala Val Asn Phe Asn Ser Ala Asn Ile Thr
             20                  25                  30
acg agt ttg aat aat tcc tct atc gtg ttt aag ggg gcg gtc tct tta   144
Thr Ser Leu Asn Asn Ser Ser Ile Val Phe Lys Gly Ala Val Ser Leu
         35                  40                  45
gga ggg cag ttt aat tta agc aat aac tct tct tta gat ttc caa ggc   192
Gly Gly Gln Phe Asn Leu Ser Asn Asn Ser Ser Leu Asp Phe Gln Gly
     50                  55                  60
tct agc gct atc acc tct aac acg gcg ttt aat ttc tat gat aac gct   240
Ser Ser Ala Ile Thr Ser Asn Thr Ala Phe Asn Phe Tyr Asp Asn Ala
 65                  70                  75                  80
ttt tct caa agc ccc atc act ttc cat caa gcc ctt gac att aaa gcg   288
Phe Ser Gln Ser Pro Ile Thr Phe His Gln Ala Leu Asp Ile Lys Ala
                 85                  90                  95
ccc tta agt ttg gga ggc aac ctt tta aac cct aac aac agc agc gtg   336
Pro Leu Ser Leu Gly Gly Asn Leu Leu Asn Pro Asn Asn Ser Ser Val
            100                 105                 110
ctg gat tta aaa aac agc cag ctt gtt ttt ggc gat caa ggg agt ttg   384
Leu Asp Leu Lys Asn Ser Gln Leu Val Phe Gly Asp Gln Gly Ser Leu
        115                 120                 125
aat atc gct aac att gat tta cta agc gat cta aat gat aat aaa aat   432
Asn Ile Ala Asn Ile Asp Leu Leu Ser Asp Leu Asn Asp Asn Lys Asn
    130                 135                 140
cgt gtg tat aac atc att caa gcg gac atg aat agt aat tgg tat gag   480
Arg Val Tyr Asn Ile Ile Gln Ala Asp Met Asn Ser Asn Trp Tyr Glu
145                 150                 155                 160
cgt atc agc ttc ttt ggc atg cac atc aat gac ggg att tat gat gct   528
Arg Ile Ser Phe Phe Gly Met His Ile Asn Asp Gly Ile Tyr Asp Ala
                165                 170                 175
aaa aac caa act tat agt ttc act aac ccc ctt aat aac gcc cta aaa   576
Lys Asn Gln Thr Tyr Ser Phe Thr Asn Pro Leu Asn Asn Ala Leu Lys
            180                 185                 190
atc acc gag agc ttt aaa gac aac caa cta agc gtt acg ctc tct caa   624
Ile Thr Glu Ser Phe Lys Asp Asn Gln Leu Ser Val Thr Leu Ser Gln
        195                 200                 205
atc ccg ggt att aaa aac acg ctc tat aac att ggc tct gaa att ttt   672
Ile Pro Gly Ile Lys Asn Thr Leu Tyr Asn Ile Gly Ser Glu Ile Phe
    210                 215                 220
aac tac caa aaa gtt tat aac aac gct aat ggc gtg tat tct tat agc   720
Asn Tyr Gln Lys Val Tyr Asn Asn Ala Asn Gly Val Tyr Ser Tyr Ser
225                 230                 235                 240
gat gat gca caa ggc gtg ttt tat ctc aca                          750
Asp Asp Ala Gln Gly Val Phe Tyr Leu Thr
                245                 250

<210> 58
<211> 250
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<212> PRT
<213> Helicobacter pylori
<400> 58
Asn Ala Thr Ile Asn Asp Tyr Ala Ser Leu Ile Ala Ser Asn Gly Ser
1 5 10 15
His Leu Asn Phe Asn Gly Ala Val Asn Phe Asn Ser Ala Asn Ile Thr
20 25 30
Thr Ser Leu Asn Asn Ser Ser Ile Val Phe Lys Gly Ala Val Ser Leu
35 40 45
Gly Gly Gln Phe Asn Leu Ser Asn Asn Ser Ser Leu Asp Phe Gln Gly
50 55 60
Ser Ser Ala Ile Thr Ser Asn Thr Ala Phe Asn Phe Tyr Asp Asn Ala
65 70 75 80
Phe Ser Gln Ser Pro Ile Thr Phe His Gln Ala Leu Asp Ile Lys Ala
85 90 95
Pro Leu Ser Leu Gly Gly Asn Leu Leu Asn Pro Asn Asn Ser Ser Val
100 105 110
Leu Asp Leu Lys Asn Ser Gln Leu Val Phe Gly Asp Gln Gly Ser Leu
115 120 125
Asn Ile Ala Asn Ile Asp Leu Leu Ser Asp Leu Asn Asp Asn Lys Asn
130 135 140
Arg Val Tyr Asn Ile Ile Gln Ala Asp Met Asn Ser Asn Trp Tyr Glu
145 150 155 160
Arg Ile Ser Phe Phe Gly Met His Ile Asn Asp Gly Ile Tyr Asp Ala
165 170 175
Lys Asn Gln Thr Tyr Ser Phe Thr Asn Pro Leu Asn Asn Ala Leu Lys
180 185 190
Ile Thr Glu Ser Phe Lys Asp Asn Gln Leu Ser Val Thr Leu Ser Gln
195 200 205
Ile Pro Gly Ile Lys Asn Thr Leu Tyr Asn Ile Gly Ser Glu Ile Phe
210 215 220
Asn Tyr Gln Lys Val Tyr Asn Asn Ala Asn Gly Val Tyr Ser Tyr Ser
225 230 235 240
Asp Asp Ala Gln Gly Val Phe Tyr Leu Thr
245 250

<210> 59
<211> 989
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(987)
<400> 59
ctt atc aat ttc aaa ggg aat acg aat ttt aat caa gcc acg ctc aat 48
Leu Ile Asn Phe Lys Gly Asn Thr Asn Phe Asn Gln Ala Thr Leu Asn
1 5 10 15
tta agg gct aaa aat atc cat atc aat ttc caa ggc gtt tct act ttt 96
Leu Arg Ala Lys Asn Ile His Ile Asn Phe Gln Gly Val Ser Thr Phe
20 25 30
aaa caa aac tct acg atg aat tta gct gaa agt tcc caa gcg agc ttt 144
Lys Gln Asn Ser Thr Met Asn Leu Ala Glu Ser Ser Gln Ala Ser Phe
35 40 45
aac gct ctt aaa gtg gaa ggg gaa acg aat ttc aat ctc aat aac tca 192
Asn Ala Leu Lys Val Glu Gly Glu Thr Asn Phe Asn Leu Asn Asn Ser
50 55 60
agc ttg ttg aat ttc aat ggc aat agc gtt ttc aac gct cct gtg agt 240
Ser Leu Leu Asn Phe Asn Gly Asn Ser Val Phe Asn Ala Pro Val Ser
65 70 75 80
ttt tat gct aat cat tct caa att tct ttc act aaa tta gcg act ttt 288
Phe Tyr Ala Asn His Ser Gln Ile Ser Phe Thr Lys Leu Ala Thr Phe
85 90 95

```
aat tct gac gct tct ttt gat tta agc aac aac agc acc ctg aat ttt   336
Asn Ser Asp Ala Ser Phe Asp Leu Ser Asn Asn Ser Thr Leu Asn Phe
            100                 105                 110
caa agc gtt ctt tta aat ggt gct cta aac ctt tta ggc aat ggc agt   384
Gln Ser Val Leu Leu Asn Gly Ala Leu Asn Leu Leu Gly Asn Gly Ser
        115                 120                 125
aac aat cta gcg atc aac gct aaa ggg aat ttt agt ttt ggg tct aaa   432
Asn Asn Leu Ala Ile Asn Ala Lys Gly Asn Phe Ser Phe Gly Ser Lys
    130                 135                 140
ggg att ttg aat ctg tct tat atg aat cta ttt ggg ggg gat aaa aaa   480
Gly Ile Leu Asn Leu Ser Tyr Met Asn Leu Phe Gly Gly Asp Lys Lys
145                 150                 155                 160
act tcc gtt tat gat gtg ttg caa gcc caa aat att gat ggc tta atg   528
Thr Ser Val Tyr Asp Val Leu Gln Ala Gln Asn Ile Asp Gly Leu Met
                165                 170                 175
ggg aat aac ggc tat gag aag atc cgt ttt tat ggc ata cag att gac   576
Gly Asn Asn Gly Tyr Glu Lys Ile Arg Phe Tyr Gly Ile Gln Ile Asp
            180                 185                 190
aag gct gat tac tcg ttt gat aac ggc gtt cat tct tgg aga ttc act   624
Lys Ala Asp Tyr Ser Phe Asp Asn Gly Val His Ser Trp Arg Phe Thr
        195                 200                 205
aac ccg ctc aat acg act gaa acg att aca gaa acc ttg cat aac aac   672
Asn Pro Leu Asn Thr Thr Glu Thr Ile Thr Glu Thr Leu His Asn Asn
    210                 215                 220
cgc ttg aaa gtg cag atc tct caa aac ggc gtt tct aat aat aag atg   720
Arg Leu Lys Val Gln Ile Ser Gln Asn Gly Val Ser Asn Asn Lys Met
225                 230                 235                 240
ttc aat ctc gct cct agc ttg tat gat tac caa aaa aac cct tat aat   768
Phe Asn Leu Ala Pro Ser Leu Tyr Asp Tyr Gln Lys Asn Pro Tyr Asn
                245                 250                 255
gaa acc gag aat tcc tat aat tac aca agc gat aag gtt ggc act tat   816
Glu Thr Glu Asn Ser Tyr Asn Tyr Thr Ser Asp Lys Val Gly Thr Tyr
            260                 265                 270
tat tta acg agc aat atc aaa ggc ttt aat caa aac aat aaa aca ccc   864
Tyr Leu Thr Ser Asn Ile Lys Gly Phe Asn Gln Asn Asn Lys Thr Pro
        275                 280                 285
ggg act tat aac gcg caa aac caa ccc tta caa gcc tta cac att tac   912
Gly Thr Tyr Asn Ala Gln Asn Gln Pro Leu Gln Ala Leu His Ile Tyr
    290                 295                 300
aat cag gct atc act aag caa gat ttg aac atg atc gcc agt ttg ggt   960
Asn Gln Ala Ile Thr Lys Gln Asp Leu Asn Met Ile Ala Ser Leu Gly
305                 310                 315                 320
aag gag ttt ttg cct aaa ata gcc aat ct                           989
Lys Glu Phe Leu Pro Lys Ile Ala Asn
                325
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<210> 60
<211> 329
<212> PRT
<213> Helicobacter pylori
<400> 60

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Leu Ile Asn Phe Lys Gly Asn Thr Asn Phe Asn Gln Ala Thr Leu Asn
  1               5                  10                  15
Leu Arg Ala Lys Asn Ile His Ile Asn Phe Gln Gly Val Ser Thr Phe
            20                  25                  30
Lys Gln Asn Ser Thr Met Asn Leu Ala Glu Ser Ser Gln Ala Ser Phe
        35                  40                  45
Asn Ala Leu Lys Val Glu Gly Glu Thr Asn Phe Asn Leu Asn Asn Ser
    50                  55                  60
Ser Leu Leu Asn Phe Asn Gly Asn Ser Val Phe Asn Ala Pro Val Ser
65                  70                  75                  80
Phe Tyr Ala Asn His Ser Gln Ile Ser Phe Thr Lys Leu Ala Thr Phe
```

```
                85                  90                  95
Asn Ser Asp Ala Ser Phe Asp Leu Ser Asn Asn Ser Thr Leu Asn Phe
            100                 105                 110
Gln Ser Val Leu Leu Asn Gly Ala Leu Asn Leu Leu Gly Asn Gly Ser
        115                 120                 125
Asn Asn Leu Ala Ile Asn Ala Lys Gly Asn Phe Ser Phe Gly Ser Lys
    130                 135                 140
Gly Ile Leu Asn Leu Ser Tyr Met Asn Leu Phe Gly Gly Asp Lys Lys
145                 150                 155                 160
Thr Ser Val Tyr Asp Val Leu Gln Ala Gln Asn Ile Asp Gly Leu Met
                165                 170                 175
Gly Asn Asn Gly Tyr Glu Lys Ile Arg Phe Tyr Gly Ile Gln Ile Asp
            180                 185                 190
Lys Ala Asp Tyr Ser Phe Asp Asn Gly Val His Ser Trp Arg Phe Thr
        195                 200                 205
Asn Pro Leu Asn Thr Thr Glu Thr Ile Thr Glu Thr Leu His Asn Asn
    210                 215                 220
Arg Leu Lys Val Gln Ile Ser Gln Asn Gly Val Ser Asn Asn Lys Met
225                 230                 235                 240
Phe Asn Leu Ala Pro Ser Leu Tyr Asp Tyr Gln Lys Asn Pro Tyr Asn
                245                 250                 255
Glu Thr Glu Asn Ser Tyr Asn Tyr Thr Ser Asp Lys Val Gly Thr Tyr
            260                 265                 270
Tyr Leu Thr Ser Asn Ile Lys Gly Phe Asn Gln Asn Asn Lys Thr Pro
        275                 280                 285
Gly Thr Tyr Asn Ala Gln Asn Gln Pro Leu Gln Ala Leu His Ile Tyr
    290                 295                 300
Asn Gln Ala Ile Thr Lys Gln Asp Leu Asn Met Ile Ala Ser Leu Gly
305                 310                 315                 320
Lys Glu Phe Leu Pro Lys Ile Ala Asn
                325
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<210> 61
<211> 357
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(357)
<400> 61

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tta atg ctt aaa gac acg cat tta agg cat gtg aaa gat ctc aaa agc   48
Leu Met Leu Lys Asp Thr His Leu Arg His Val Lys Asp Leu Lys Ser
  1               5                  10                  15
ttt tta acg cat gcc aga aaa aac ttg cct ttc acg gct aaa att gaa   96
Phe Leu Thr His Ala Arg Lys Asn Leu Pro Phe Thr Ala Lys Ile Glu
             20                  25                  30
att gaa tgc gaa agc ttt gaa gag gcc aaa aac gcc atg aat gcg gga   144
Ile Glu Cys Glu Ser Phe Glu Glu Ala Lys Asn Ala Met Asn Ala Gly
         35                  40                  45
gcg gat att gtg atg tgc gat aat ttg agc gtt tta gag act aaa gaa   192
Ala Asp Ile Val Met Cys Asp Asn Leu Ser Val Leu Glu Thr Lys Glu
     50                  55                  60
att gcc gct tat aga gat gcg cat tat ccc ttt gtt tta ctg gaa gcg   240
Ile Ala Ala Tyr Arg Asp Ala His Tyr Pro Phe Val Leu Leu Glu Ala
 65                  70                  75                  80
agc ggg aac att tca cta gag agc att aac gct tac gct aaa agc ggc   288
Ser Gly Asn Ile Ser Leu Glu Ser Ile Asn Ala Tyr Ala Lys Ser Gly
                 85                  90                  95
gtg gat gcc att agc gta ggg gct tta atc cat caa gcc act ttt att   336
Val Asp Ala Ile Ser Val Gly Ala Leu Ile His Gln Ala Thr Phe Ile
            100                 105                 110
gac atg cac atg aaa atg gct                                      357
```

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Asp Met His Met Lys Met Ala
        115
<210> 62
<211> 119
<212> PRT
<213> Helicobacter pylori
<400> 62
Leu Met Leu Lys Asp Thr His Leu Arg His Val Lys Asp Leu Lys Ser
  1               5                  10                  15
Phe Leu Thr His Ala Arg Lys Asn Leu Pro Phe Thr Ala Lys Ile Glu
            20                  25                  30
Ile Glu Cys Glu Ser Phe Glu Glu Ala Lys Asn Ala Met Asn Ala Gly
        35                  40                  45
Ala Asp Ile Val Met Cys Asp Asn Leu Ser Val Leu Glu Thr Lys Glu
    50                  55                  60
Ile Ala Ala Tyr Arg Asp Ala His Tyr Pro Phe Val Leu Leu Glu Ala
65                  70                  75                  80
Ser Gly Asn Ile Ser Leu Glu Ser Ile Asn Ala Tyr Ala Lys Ser Gly
                85                  90                  95
Val Asp Ala Ile Ser Val Gly Ala Leu Ile His Gln Ala Thr Phe Ile
            100                 105                 110
Asp Met His Met Lys Met Ala
        115
<210> 63
<211> 437
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(435)
<400> 63
gtt ggc aat cta agg gat tta aac ccc ttg gat ttc agc gtg gat cat   48
Val Gly Asn Leu Arg Asp Leu Asn Pro Leu Asp Phe Ser Val Asp His
  1               5                  10                  15
gtg gat ttg gaa tgg ttt gaa acg agg aaa aaa atc gct cgt ttt aaa   96
Val Asp Leu Glu Trp Phe Glu Thr Arg Lys Lys Ile Ala Arg Phe Lys
            20                  25                  30
acc agg caa ggc aaa gac ata gcc ata cgc ctt aaa gac gct ccc aag  144
Thr Arg Gln Gly Lys Asp Ile Ala Ile Arg Leu Lys Asp Ala Pro Lys
        35                  40                  45
ttg ggg ctc tct caa ggg gat att tta ttt aaa gaa gag aag gaa att  192
Leu Gly Leu Ser Gln Gly Asp Ile Leu Phe Lys Glu Glu Lys Glu Ile
    50                  55                  60
atc gcc gtt aat atc ttg gat tct gaa gtc att cac atc caa gcc aag  240
Ile Ala Val Asn Ile Leu Asp Ser Glu Val Ile His Ile Gln Ala Lys
65                  70                  75                  80
agc gtg gca gaa gta gcg aaa ata tgc tat gaa ata gga aac cgc cat  288
Ser Val Ala Glu Val Ala Lys Ile Cys Tyr Glu Ile Gly Asn Arg His
                85                  90                  95
gcg gct tta tac tat ggc gag tct caa ttt gaa ttt aaa aca cca ttt  336
Ala Ala Leu Tyr Tyr Gly Glu Ser Gln Phe Glu Phe Lys Thr Pro Phe
            100                 105                 110
gaa aag ccc acg cta gcg tta tta gaa aag cta ggg gtt caa aat cgt  384
Glu Lys Pro Thr Leu Ala Leu Leu Glu Lys Leu Gly Val Gln Asn Arg
        115                 120                 125
gtt tta agt tca aaa ttg gat tcc aaa gaa cgc tta acc gtg agc atg  432
Val Leu Ser Ser Lys Leu Asp Ser Lys Glu Arg Leu Thr Val Ser Met
    130                 135                 140
ccc ca                                                          437
Pro
145
```

<210> 64
<211> 145
<212> PRT
<213> Helicobacter pylori
<400> 64

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Val Gly Asn Leu Arg Asp Leu Asn Pro Leu Asp Phe Ser Val Asp His
 1               5                  10                  15
Val Asp Leu Glu Trp Phe Glu Thr Arg Lys Lys Ile Ala Arg Phe Lys
            20                  25                  30
Thr Arg Gln Gly Lys Asp Ile Ala Ile Arg Leu Lys Asp Ala Pro Lys
        35                  40                  45
Leu Gly Leu Ser Gln Gly Asp Ile Leu Phe Lys Glu Glu Lys Glu Ile
    50                  55                  60
Ile Ala Val Asn Ile Leu Asp Ser Glu Val Ile His Ile Gln Ala Lys
65                  70                  75                  80
Ser Val Ala Glu Val Ala Lys Ile Cys Tyr Glu Ile Gly Asn Arg His
                85                  90                  95
Ala Ala Leu Tyr Tyr Gly Glu Ser Gln Phe Glu Phe Lys Thr Pro Phe
            100                 105                 110
Glu Lys Pro Thr Leu Ala Leu Leu Glu Lys Leu Gly Val Gln Asn Arg
        115                 120                 125
Val Leu Ser Ser Lys Leu Asp Ser Lys Glu Arg Leu Thr Val Ser Met Pro
    130                 135                 140                 145
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<210> 65
<211> 831
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(831)
<400> 65

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agc act ggt gat gtt agt gaa caa ata gaa cta gaa caa gaa aaa caa   48
Ser Thr Gly Asp Val Ser Glu Gln Ile Glu Leu Glu Gln Glu Lys Gln
 1               5                  10                  15
aag acg agc aat ata gag act aac aat caa ata aaa gta gaa caa gaa   96
Lys Thr Ser Asn Ile Glu Thr Asn Asn Gln Ile Lys Val Glu Gln Glu
            20                  25                  30
aaa caa aag aca agc aat ata gag act aat aat caa ata aaa gta gaa   144
Lys Gln Lys Thr Ser Asn Ile Glu Thr Asn Asn Gln Ile Lys Val Glu
        35                  40                  45
caa gaa caa caa aag aca agc aat aca cag aaa gat ttg gtt aaa gaa   192
Gln Glu Gln Gln Lys Thr Ser Asn Thr Gln Lys Asp Leu Val Lys Glu
    50                  55                  60
cag aaa gat ttg gtt aaa gaa cag aaa gat ttg gtt aaa gaa cag aaa   240
Gln Lys Asp Leu Val Lys Glu Gln Lys Asp Leu Val Lys Glu Gln Lys
65                  70                  75                  80
gat ttg gtt aaa gaa cag aaa gat ttg gtt aaa aca cag aaa gat ttc   288
Asp Leu Val Lys Glu Gln Lys Asp Leu Val Lys Thr Gln Lys Asp Phe
                85                  90                  95
att aaa tat gta gaa caa aat tgc caa gaa aat cat aat caa ttc ttt   336
Ile Lys Tyr Val Glu Gln Asn Cys Gln Glu Asn His Asn Gln Phe Phe
            100                 105                 110
att gaa aaa gga gga att aag gct ggt att ggt ata gaa gta gaa gct   384
Ile Glu Lys Gly Gly Ile Lys Ala Gly Ile Gly Ile Glu Val Glu Ala
        115                 120                 125
gaa tgc aaa acc cct aaa cct gca aaa acc aat caa acc cct atc cag   432
Glu Cys Lys Thr Pro Lys Pro Ala Lys Thr Asn Gln Thr Pro Ile Gln
    130                 135                 140
cca aaa cac ctc cca aac tct aaa caa ccc cgc tct caa aga gga tca   480
Pro Lys His Leu Pro Asn Ser Lys Gln Pro Arg Ser Gln Arg Gly Ser
145                 150                 155                 160
```

```
aaa gcg caa gag ctt atc gct tat ttg caa aaa gag cta gaa ttt ctg   528
Lys Ala Gln Glu Leu Ile Ala Tyr Leu Gln Lys Glu Leu Glu Phe Leu
                165                 170                 175
ccc tat tcg caa aaa gct atc gct aaa caa gtg gat ttt tac agg cca   576
Pro Tyr Ser Gln Lys Ala Ile Ala Lys Gln Val Asp Phe Tyr Arg Pro
            180                 185                 190
agt tct atc gct tat tta gaa cta gat cct aga gat ttt aag gtt aca   624
Ser Ser Ile Ala Tyr Leu Glu Leu Asp Pro Arg Asp Phe Lys Val Thr
        195                 200                 205
gaa gaa tgg caa aaa gaa aat cta aaa ata cgc tct aaa gct caa gct   672
Glu Glu Trp Gln Lys Glu Asn Leu Lys Ile Arg Ser Lys Ala Gln Ala
    210                 215                 220
aaa atg ctt gaa atg aga aac cca caa gcc cac ctt tca aac tct caa   720
Lys Met Leu Glu Met Arg Asn Pro Gln Ala His Leu Ser Asn Ser Gln
225                 230                 235                 240
agc ctt ttg ttc gtt caa aaa ata ttt gct gat gtt aat aaa gaa ata   768
Ser Leu Leu Phe Val Gln Lys Ile Phe Ala Asp Val Asn Lys Glu Ile
                245                 250                 255
gaa gca gtt gct aat act gaa aag aaa gca gaa aaa gcg ggt tat ggt   816
Glu Ala Val Ala Asn Thr Glu Lys Lys Ala Glu Lys Ala Gly Tyr Gly
            260                 265                 270
tat agt aaa agg atg                                              831
Tyr Ser Lys Arg Met
        275
```

<210> 66
<211> 277
<212> PRT
<213> Helicobacter pylori
<400> 66

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Ser Thr Gly Asp Val Ser Glu Gln Ile Glu Leu Glu Gln Glu Lys Gln
  1               5                  10                  15
Lys Thr Ser Asn Ile Glu Thr Asn Asn Gln Ile Lys Val Glu Gln Glu
            20                  25                  30
Lys Gln Lys Thr Ser Asn Ile Glu Thr Asn Asn Gln Ile Lys Val Glu
        35                  40                  45
Gln Glu Gln Gln Lys Thr Ser Asn Thr Gln Lys Asp Leu Val Lys Glu
    50                  55                  60
Gln Lys Asp Leu Val Lys Glu Gln Lys Asp Leu Val Lys Glu Gln Lys
65                  70                  75                  80
Asp Leu Val Lys Glu Gln Lys Asp Leu Val Lys Thr Gln Lys Asp Phe
                85                  90                  95
Ile Lys Tyr Val Glu Gln Asn Cys Gln Glu Asn His Asn Gln Phe Phe
            100                 105                 110
Ile Glu Lys Gly Gly Ile Lys Ala Gly Ile Gly Ile Glu Val Glu Ala
        115                 120                 125
Glu Cys Lys Thr Pro Lys Pro Ala Lys Thr Asn Gln Thr Pro Ile Gln
    130                 135                 140
Pro Lys His Leu Pro Asn Ser Lys Gln Pro Arg Ser Gln Arg Gly Ser
145                 150                 155                 160
Lys Ala Gln Glu Leu Ile Ala Tyr Leu Gln Lys Glu Leu Glu Phe Leu
                165                 170                 175
Pro Tyr Ser Gln Lys Ala Ile Ala Lys Gln Val Asp Phe Tyr Arg Pro
            180                 185                 190
Ser Ser Ile Ala Tyr Leu Glu Leu Asp Pro Arg Asp Phe Lys Val Thr
        195                 200                 205
Glu Glu Trp Gln Lys Glu Asn Leu Lys Ile Arg Ser Lys Ala Gln Ala
    210                 215                 220
Lys Met Leu Glu Met Arg Asn Pro Gln Ala His Leu Ser Asn Ser Gln
225                 230                 235                 240
Ser Leu Leu Phe Val Gln Lys Ile Phe Ala Asp Val Asn Lys Glu Ile
                245                 250                 255
```

```
Glu Ala Val Ala Asn Thr Glu Lys Lys Ala Glu Lys Ala Gly Tyr Gly
            260                 265                 270
Tyr Ser Lys Arg Met
        275
<210> 67
<211> 915
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(915)
<400> 67
aaa gaa tgg att gtt gca ttt gat gaa gac gcc cct aaa ttt gaa gct   48
Lys Glu Trp Ile Val Ala Phe Asp Glu Asp Ala Pro Lys Phe Glu Ala
 1               5                  10                  15
agt ggg gaa tat tgc gtg agc acg gat agt ttt gtc atc acg ccc tta   96
Ser Gly Glu Tyr Cys Val Ser Thr Asp Ser Phe Val Ile Thr Pro Leu
            20                  25                  30
att ttt aat ggg ggc gat ata ggc aag ctt tgc gtt tgc ggg agt gcg   144
Ile Phe Asn Gly Gly Asp Ile Gly Lys Leu Cys Val Cys Gly Ser Ala
        35                  40                  45
aat gat gtg agc gtg caa ggg ggc gaa cct ttg tat ttg aat atg ggt   192
Asn Asp Val Ser Val Gln Gly Gly Glu Pro Leu Tyr Leu Asn Met Gly
    50                  55                  60
ttt att tta gaa gaa ggc tta gaa att tct ctt tta aaa caa att tta   240
Phe Ile Leu Glu Glu Gly Leu Glu Ile Ser Leu Leu Lys Gln Ile Leu
65                  70                  75                  80
caa tcc ata caa aaa gaa ttg ttt aaa gcc aac ctg aaa ctc ctc tcc   288
Gln Ser Ile Gln Lys Glu Leu Phe Lys Ala Asn Leu Lys Leu Leu Ser
                85                  90                  95
cta gac act aaa gtc gtg cca aag ggg agc gtg gat aag ctt ttt atc   336
Leu Asp Thr Lys Val Val Pro Lys Gly Ser Val Asp Lys Leu Phe Ile
            100                 105                 110
aac aca acc tgc att ggt aaa atc atc aag cca ggg att tct tcg tac   384
Asn Thr Thr Cys Ile Gly Lys Ile Ile Lys Pro Gly Ile Ser Ser Tyr
        115                 120                 125
cat tta caa caa ggg caa gcc att atc cta agc gac act atc gcc aat   432
His Leu Gln Gln Gly Gln Ala Ile Ile Leu Ser Asp Thr Ile Ala Asn
    130                 135                 140
cat ggg gca agc tta ttt gcg atg cgt aat gaa atc aag ctt aaa acg   480
His Gly Ala Ser Leu Phe Ala Met Arg Asn Glu Ile Lys Leu Lys Thr
145                 150                 155                 160
aat cta gaa agc gat tgc caa ctg ctc tat ccc tta tta aaa ccc cta   528
Asn Leu Glu Ser Asp Cys Gln Leu Leu Tyr Pro Leu Leu Lys Pro Leu
                165                 170                 175
ttt tta agc gat ctc aaa att gat gct tta aga gat gcg act agg ggc   576
Phe Leu Ser Asp Leu Lys Ile Asp Ala Leu Arg Asp Ala Thr Arg Gly
            180                 185                 190
ggg tta gcg agc gtg ctg aac gaa tgg gcg aac agc tct aga gtg aaa   624
Gly Leu Ala Ser Val Leu Asn Glu Trp Ala Asn Ser Ser Arg Val Lys
        195                 200                 205
atc gtt ata gaa gaa gaa aaa atc ccc tta aaa gaa gaa acg aaa ggg   672
Ile Val Ile Glu Glu Glu Lys Ile Pro Leu Lys Glu Glu Thr Lys Gly
    210                 215                 220
att tgt gag att tta ggg tta gaa ccc tac gcg cta gcc aat gag ggg   720
Ile Cys Glu Ile Leu Gly Leu Glu Pro Tyr Ala Leu Ala Asn Glu Gly
225                 230                 235                 240
gtg ttt gtt tta gcg ctc aat caa aaa gac gcc cct aaa gcc tta gaa   768
Val Phe Val Leu Ala Leu Asn Gln Lys Asp Ala Pro Lys Ala Leu Glu
                245                 250                 255
att tta aaa agt aac gaa aaa gct aaa aac gct tgc gtg att ggc aaa   816
```

```
Ile Leu Lys Ser Asn Glu Lys Ala Lys Asn Ala Cys Val Ile Gly Lys
            260                 265                 270
gtg ttt gaa aac cct tat cct agc gtg gtt tta aag aac gca tgg ggt   864
Val Phe Glu Asn Pro Tyr Pro Ser Val Val Leu Lys Asn Ala Trp Gly
        275                 280                 285
ttt gaa agg att tta gag gtg cca gag ggc gaa tta ttg cct agg att   912
Phe Glu Arg Ile Leu Glu Val Pro Glu Gly Glu Leu Leu Pro Arg Ile
    290                 295                 300
                                                                  915
tgt
Cys
305
<210> 68
<211> 305
<212> PRT
<213> Helicobacter pylori
<400> 68
Lys Glu Trp Ile Val Ala Phe Asp Glu Asp Ala Pro Lys Phe Glu Ala
  1               5                  10                  15
Ser Gly Glu Tyr Cys Val Ser Thr Asp Ser Phe Val Ile Thr Pro Leu
            20                  25                  30
Ile Phe Asn Gly Gly Asp Ile Gly Lys Leu Cys Val Cys Gly Ser Ala
        35                  40                  45
Asn Asp Val Ser Val Gln Gly Gly Glu Pro Leu Tyr Leu Asn Met Gly
    50                  55                  60
Phe Ile Leu Glu Glu Gly Leu Glu Ile Ser Leu Leu Lys Gln Ile Leu
65                  70                  75                  80
Gln Ser Ile Gln Lys Glu Leu Phe Lys Ala Asn Leu Lys Leu Leu Ser
                85                  90                  95
Leu Asp Thr Lys Val Val Pro Lys Gly Ser Val Asp Lys Leu Phe Ile
            100                 105                 110
Asn Thr Thr Cys Ile Gly Lys Ile Ile Lys Pro Gly Ile Ser Ser Tyr
        115                 120                 125
His Leu Gln Gln Gly Gln Ala Ile Ile Leu Ser Asp Thr Ile Ala Asn
    130                 135                 140
His Gly Ala Ser Leu Phe Ala Met Arg Asn Glu Ile Lys Leu Lys Thr
145                 150                 155                 160
Asn Leu Glu Ser Asp Cys Gln Leu Leu Tyr Pro Leu Leu Lys Pro Leu
                165                 170                 175
Phe Leu Ser Asp Leu Lys Ile Asp Ala Leu Arg Asp Ala Thr Arg Gly
            180                 185                 190
Gly Leu Ala Ser Val Leu Asn Glu Trp Ala Asn Ser Ser Arg Val Lys
        195                 200                 205
Ile Val Ile Glu Glu Glu Lys Ile Pro Leu Lys Glu Glu Thr Lys Gly
    210                 215                 220
Ile Cys Glu Ile Leu Gly Leu Glu Pro Tyr Ala Leu Ala Asn Glu Gly
225                 230                 235                 240
Val Phe Val Leu Ala Leu Asn Gln Lys Asp Ala Pro Lys Ala Leu Glu
                245                 250                 255
Ile Leu Lys Ser Asn Glu Lys Ala Lys Asn Ala Cys Val Ile Gly Lys
            260                 265                 270
Val Phe Glu Asn Pro Tyr Pro Ser Val Val Leu Lys Asn Ala Trp Gly
        275                 280                 285
Phe Glu Arg Ile Leu Glu Val Pro Glu Gly Glu Leu Leu Pro Arg Ile
    290                 295                 300
Cys
305
<210> 69
<211> 1977
<212> DNA
<213> Helicobacter pylori
<220>
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<221> CDS
<222> (1)..(1977)
<400> 69

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ttg aat ttg ctc agc caa atc cct aaa gat tta ggc gtg tgc aag gat   48
Leu Asn Leu Leu Ser Gln Ile Pro Lys Asp Leu Gly Val Cys Lys Asp
  1               5                  10                  15
tgc ttg aga gaa atc agg gat aaa aac tcc ccc tat ttt cat tac gct   96
Cys Leu Arg Glu Ile Arg Asp Lys Asn Ser Pro Tyr Phe His Tyr Ala
             20                  25                  30
ttc aat tct tgc gcg aag tgt ggg gcg aga tac agc ctt tta aac gct  144
Phe Asn Ser Cys Ala Lys Cys Gly Ala Arg Tyr Ser Leu Leu Asn Ala
         35                  40                  45
ttg ccc tat gac aga gaa aac tcc gcc cta aaa ccc ttc aaa ctc tgc  192
Leu Pro Tyr Asp Arg Glu Asn Ser Ala Leu Lys Pro Phe Lys Leu Cys
     50                  55                  60
gat ttt tgt gct tct atc tat caa gac ccc acc aat aag cgc ttc cac  240
Asp Phe Cys Ala Ser Ile Tyr Gln Asp Pro Thr Asn Lys Arg Phe His
 65                  70                  75                  80
att caa ggc atc agc tgc aaa aag tgc ggt atc gcg ctc aat tac aag  288
Ile Gln Gly Ile Ser Cys Lys Lys Cys Gly Ile Ala Leu Asn Tyr Lys
                 85                  90                  95
cga ttc aaa aac gat gac gct ctt tta gaa tgc gct aaa gac att caa  336
Arg Phe Lys Asn Asp Asp Ala Leu Leu Glu Cys Ala Lys Asp Ile Gln
            100                 105                 110
aag ggt aaa atc atc gct ctt aaa ggt ttg gga ggc ttt gct ctc ttg  384
Lys Gly Lys Ile Ile Ala Leu Lys Gly Leu Gly Gly Phe Ala Leu Leu
        115                 120                 125
tgc gat gga agg aat ttt caa acc ata gaa aga tta cgg ctt tta aaa  432
Cys Asp Gly Arg Asn Phe Gln Thr Ile Glu Arg Leu Arg Leu Leu Lys
    130                 135                 140
aac cgc ccc cta aag cct ttc gca ctc atg ttt aaa gat ttg aac aca  480
Asn Arg Pro Leu Lys Pro Phe Ala Leu Met Phe Lys Asp Leu Asn Thr
145                 150                 155                 160
gcc aaa cag cat gcg ttt ttg aac gcg tta gaa tgc gag agc tta att  528
Ala Lys Gln His Ala Phe Leu Asn Ala Leu Glu Cys Glu Ser Leu Ile
                165                 170                 175
tct aca agc gcc ccc att ctt tta gcg cgt aaa aaa cct gat ata aaa  576
Ser Thr Ser Ala Pro Ile Leu Leu Ala Arg Lys Lys Pro Asp Ile Lys
            180                 185                 190
tta gcc ccc aat atc gct aaa aac tcc ccc ttt tat ggc gtg att ttg  624
Leu Ala Pro Asn Ile Ala Lys Asn Ser Pro Phe Tyr Gly Val Ile Leu
        195                 200                 205
ccc tat acc cct ttg cat gct tta ttg ctg gat tta ttg gat ttc cct  672
Pro Tyr Thr Pro Leu His Ala Leu Leu Leu Asp Leu Leu Asp Phe Pro
    210                 215                 220
att gtg ttc acg agc gcg aat ttc agc tcc ctc cct tta gcg agc gat  720
Ile Val Phe Thr Ser Ala Asn Phe Ser Ser Leu Pro Leu Ala Ser Asp
225                 230                 235                 240
gag gct gag att gac gcc ttg agt ttc att ttt gat ttt aag ctc acg  768
Glu Ala Glu Ile Asp Ala Leu Ser Phe Ile Phe Asp Phe Lys Leu Thr
                245                 250                 255
cac aac cgc gct atc atc cat agg att gat gac agc atc gtg cag cat  816
His Asn Arg Ala Ile Ile His Arg Ile Asp Asp Ser Ile Val Gln His
            260                 265                 270
gtg gat aat gcc att cgc ccc atg cgt ttg gct agg ggg ttt gcc ccc  864
Val Asp Asn Ala Ile Arg Pro Met Arg Leu Ala Arg Gly Phe Ala Pro
        275                 280                 285
ctt tac ctc acc ttg cct aaa cgc tct aat ggt tcg cca aaa aag att  912
Leu Tyr Leu Thr Leu Pro Lys Arg Ser Asn Gly Ser Pro Lys Lys Ile
    290                 295                 300
tta gcg ctt gga gcg caa caa aaa ggg cat ttt agc tta ttg gat agc  960
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```
Leu Ala Leu Gly Ala Gln Gln Lys Gly His Phe Ser Leu Leu Asp Ser
305                 310                 315                 320
gga act tcc att ctt tta ctc tcg cct ttt tgt ggg gat ttg agc gtt   1008
Gly Thr Ser Ile Leu Leu Leu Ser Pro Phe Cys Gly Asp Leu Ser Val
                325                 330                 335
tta gaa aat gaa aaa cac ttt aaa gaa act ttg aat ttt ttc tta aaa   1056
Leu Glu Asn Glu Lys His Phe Lys Glu Thr Leu Asn Phe Phe Leu Lys
            340                 345                 350
acc tat gat ttt aaa ccc acc atc tta gct tgc gac aag cat caa aac   1104
Thr Tyr Asp Phe Lys Pro Thr Ile Leu Ala Cys Asp Lys His Gln Asn
        355                 360                 365
tac acc acc act caa atg gct ttt gat ttt aat acg ccc ttg ttg caa   1152
Tyr Thr Thr Thr Gln Met Ala Phe Asp Phe Asn Thr Pro Leu Leu Gln
    370                 375                 380
gtc cag cac cac cat gcc cac ttt tta gcg agc gtc tta gac gca ttg   1200
Val Gln His His His Ala His Phe Leu Ala Ser Val Leu Asp Ala Leu
385                 390                 395                 400
tta caa gat ccg cat tta aat cac ccc ttt ata ggc att gtc tgg gat   1248
Leu Gln Asp Pro His Leu Asn His Pro Phe Ile Gly Ile Val Trp Asp
                405                 410                 415
ggg agt ggg gct tat gaa aat aag att tat ggg gcg gag tgt ttt gtg   1296
Gly Ser Gly Ala Tyr Glu Asn Lys Ile Tyr Gly Ala Glu Cys Phe Val
            420                 425                 430
ggg gat ttg gaa cgc att gaa gaa acc gcc agg ttt gaa gaa ttt tgg   1344
Gly Asp Leu Glu Arg Ile Glu Glu Thr Ala Arg Phe Glu Glu Phe Trp
        435                 440                 445
ctt tta ggg ggg caa aaa gcg atc aaa gag cct aga cgc ctg gtt tta   1392
Leu Leu Gly Gly Gln Lys Ala Ile Lys Glu Pro Arg Arg Leu Val Leu
    450                 455                 460
gaa atc gct tta aaa cac caa ctc aac aag ctt tta aag cgc gtt caa   1440
Glu Ile Ala Leu Lys His Gln Leu Asn Lys Leu Leu Lys Arg Val Gln
465                 470                 475                 480
aag cat ttt aaa gaa gac gaa tta gaa att ttc caa caa atg cat gac   1488
Lys His Phe Lys Glu Asp Glu Leu Glu Ile Phe Gln Gln Met His Asp
                485                 490                 495
aaa aaa att caa agc ata gcc acc aat tcc ata ggg cgt ttg ttt gat   1536
Lys Lys Ile Gln Ser Ile Ala Thr Asn Ser Ile Gly Arg Leu Phe Asp
            500                 505                 510
ata gta gcg ttt agt ttg gat tta aca gga acg att agc ttt gaa gca   1584
Ile Val Ala Phe Ser Leu Asp Leu Thr Gly Thr Ile Ser Phe Glu Ala
        515                 520                 525
gag agc ggg cag gtt tta gaa aat cta gcc tta caa agc gat gag atc   1632
Glu Ser Gly Gln Val Leu Glu Asn Leu Ala Leu Gln Ser Asp Glu Ile
    530                 535                 540
gct ttt tac cct ttt gaa atc aaa aac agc gtg gtg tgt ttg aaa gaa   1680
Ala Phe Tyr Pro Phe Glu Ile Lys Asn Ser Val Val Cys Leu Lys Glu
545                 550                 555                 560
ttt tat caa gcg ttt gaa aag gat ttg ggc gtt tta gag cct gaa cgc   1728
Phe Tyr Gln Ala Phe Glu Lys Asp Leu Gly Val Leu Glu Pro Glu Arg
                565                 570                 575
atc gct aag aaa ttt ttt aac agc cta gta gaa atc att acc gct tta   1776
Ile Ala Lys Lys Phe Phe Asn Ser Leu Val Glu Ile Ile Thr Ala Leu
            580                 585                 590
atc gtg cct ttt aaa gag cat gtg gtg gtg tgc agt ggg ggc gtg ttt   1824
Ile Val Pro Phe Lys Glu His Val Val Val Cys Ser Gly Gly Val Phe
        595                 600                 605
tgc aac caa tta tta tgc gaa caa tta gcc aaa cga ttg aga ggg cta   1872
Cys Asn Gln Leu Leu Cys Glu Gln Leu Ala Lys Arg Leu Arg Gly Leu
    610                 615                 620
aag agg cag tat ttt ttc cac aag cat ttc ccc cct aat gac agc agt   1920
Lys Arg Gln Tyr Phe Phe His Lys His Phe Pro Pro Asn Asp Ser Ser
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625 630 635 640
atc cct atc ggt caa gcc tta atg gcg tat ttc aac cct aca atc atc 1968
Ile Pro Ile Gly Gln Ala Leu Met Ala Tyr Phe Asn Pro Thr Ile Ile
645 650 655
1977
aaa aaa gga
Lys Lys Gly

<210> 70
<211> 659
<212> PRT
<213> Helicobacter pylori
<400> 70

Leu Asn Leu Leu Ser Gln Ile Pro Lys Asp Leu Gly Val Cys Lys Asp
1 5 10 15
Cys Leu Arg Glu Ile Arg Asp Lys Asn Ser Pro Tyr Phe His Tyr Ala
20 25 30
Phe Asn Ser Cys Ala Lys Cys Gly Ala Arg Tyr Ser Leu Leu Asn Ala
35 40 45
Leu Pro Tyr Asp Arg Glu Asn Ser Ala Leu Lys Pro Phe Lys Leu Cys
50 55 60
Asp Phe Cys Ala Ser Ile Tyr Gln Asp Pro Thr Asn Lys Arg Phe His
65 70 75 80
Ile Gln Gly Ile Ser Cys Lys Lys Cys Gly Ile Ala Leu Asn Tyr Lys
85 90 95
Arg Phe Lys Asn Asp Asp Ala Leu Leu Glu Cys Ala Lys Asp Ile Gln
100 105 110
Lys Gly Lys Ile Ile Ala Leu Lys Gly Leu Gly Gly Phe Ala Leu Leu
115 120 125
Cys Asp Gly Arg Asn Phe Gln Thr Ile Glu Arg Leu Arg Leu Leu Lys
130 135 140
Asn Arg Pro Leu Lys Pro Phe Ala Leu Met Phe Lys Asp Leu Asn Thr
145 150 155 160
Ala Lys Gln His Ala Phe Leu Asn Ala Leu Glu Cys Glu Ser Leu Ile
165 170 175
Ser Thr Ser Ala Pro Ile Leu Leu Ala Arg Lys Lys Pro Asp Ile Lys
180 185 190
Leu Ala Pro Asn Ile Ala Lys Asn Ser Pro Phe Tyr Gly Val Ile Leu
195 200 205
Pro Tyr Thr Pro Leu His Ala Leu Leu Leu Asp Leu Leu Asp Phe Pro
210 215 220
Ile Val Phe Thr Ser Ala Asn Phe Ser Ser Leu Pro Leu Ala Ser Asp
225 230 235 240
Glu Ala Glu Ile Asp Ala Leu Ser Phe Ile Phe Asp Phe Lys Leu Thr
245 250 255
His Asn Arg Ala Ile Ile His Arg Ile Asp Asp Ser Ile Val Gln His
260 265 270
Val Asp Asn Ala Ile Arg Pro Met Arg Leu Ala Arg Gly Phe Ala Pro
275 280 285
Leu Tyr Leu Thr Leu Pro Lys Arg Ser Asn Gly Ser Pro Lys Lys Ile
290 295 300
Leu Ala Leu Gly Ala Gln Gln Lys Gly His Phe Ser Leu Leu Asp Ser
305 310 315 320
Gly Thr Ser Ile Leu Leu Leu Ser Pro Phe Cys Gly Asp Leu Ser Val
325 330 335
Leu Glu Asn Glu Lys His Phe Lys Glu Thr Leu Asn Phe Phe Leu Lys
340 345 350
Thr Tyr Asp Phe Lys Pro Thr Ile Leu Ala Cys Asp Lys His Gln Asn
355 360 365
Tyr Thr Thr Thr Gln Met Ala Phe Asp Phe Asn Thr Pro Leu Leu Gln
370 375 380
Val Gln His His His Ala His Phe Leu Ala Ser Val Leu Asp Ala Leu
385 390 395 400

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Leu Gln Asp Pro His Leu Asn His Pro Phe Ile Gly Ile Val Trp Asp
                405                 410                 415
Gly Ser Gly Ala Tyr Glu Asn Lys Ile Tyr Gly Ala Glu Cys Phe Val
            420                 425                 430
Gly Asp Leu Glu Arg Ile Glu Glu Thr Ala Arg Phe Glu Glu Phe Trp
        435                 440                 445
Leu Leu Gly Gly Gln Lys Ala Ile Lys Glu Pro Arg Arg Leu Val Leu
    450                 455                 460
Glu Ile Ala Leu Lys His Gln Leu Asn Lys Leu Leu Lys Arg Val Gln
465                 470                 475                 480
Lys His Phe Lys Glu Asp Glu Leu Glu Ile Phe Gln Gln Met His Asp
                485                 490                 495
Lys Lys Ile Gln Ser Ile Ala Thr Asn Ser Ile Gly Arg Leu Phe Asp
            500                 505                 510
Ile Val Ala Phe Ser Leu Asp Leu Thr Gly Thr Ile Ser Phe Glu Ala
        515                 520                 525
Glu Ser Gly Gln Val Leu Glu Asn Leu Ala Leu Gln Ser Asp Glu Ile
    530                 535                 540
Ala Phe Tyr Pro Phe Glu Ile Lys Asn Ser Val Val Cys Leu Lys Glu
545                 550                 555                 560
Phe Tyr Gln Ala Phe Glu Lys Asp Leu Gly Val Leu Glu Pro Glu Arg
                565                 570                 575
Ile Ala Lys Lys Phe Phe Asn Ser Leu Val Glu Ile Ile Thr Ala Leu
            580                 585                 590
Ile Val Pro Phe Lys Glu His Val Val Val Cys Ser Gly Gly Val Phe
        595                 600                 605
Cys Asn Gln Leu Leu Cys Glu Gln Leu Ala Lys Arg Leu Arg Gly Leu
    610                 615                 620
Lys Arg Gln Tyr Phe Phe His Lys His Phe Pro Pro Asn Asp Ser Ser
625                 630                 635                 640
Ile Pro Ile Gly Gln Ala Leu Met Ala Tyr Phe Asn Pro Thr Ile Ile
                645                 650                 655
Lys Lys Gly
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<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(234)
<400> 71

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gtt gaa aaa gag cat ggt gct acg ccc cca aaa gaa gcc aaa ata ggc   48
Val Glu Lys Glu His Gly Ala Thr Pro Pro Lys Glu Ala Lys Ile Gly
  1               5                  10                  15
gtt aga aaa ttc tat cgg cat aaa aaa tgg gtg gat gca gat gtg tgg   96
Val Arg Lys Phe Tyr Arg His Lys Lys Trp Val Asp Ala Asp Val Trp
             20                  25                  30
caa atg gaa aaa tta ctg cct gga aat gaa gtc ata gga cct gcg atc  144
Gln Met Glu Lys Leu Leu Pro Gly Asn Glu Val Ile Gly Pro Ala Ile
         35                  40                  45
gtg gaa tca gat gcg acc act ttc gtg ata ccc aaa ggc ttt gcg aca  192
Val Glu Ser Asp Ala Thr Thr Phe Val Ile Pro Lys Gly Phe Ala Thr
     50                  55                  60
aga cta gac aaa cac cga ttg ttc cac ttg aaa gaa att aaa          234
Arg Leu Asp Lys His Arg Leu Phe His Leu Lys Glu Ile Lys
 65                  70                  75
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<210> 72
<211> 78
<212> PRT
<213> Helicobacter pylori

<400> 72
Val Glu Lys Glu His Gly Ala Thr Pro Pro Lys Glu Ala Lys Ile Gly
1 5 10 15
Val Arg Lys Phe Tyr Arg His Lys Lys Trp Val Asp Ala Asp Val Trp
20 25 30
Gln Met Glu Lys Leu Leu Pro Gly Asn Glu Val Ile Gly Pro Ala Ile
35 40 45
Val Glu Ser Asp Ala Thr Thr Phe Val Ile Pro Lys Gly Phe Ala Thr
50 55 60
Arg Leu Asp Lys His Arg Leu Phe His Leu Lys Glu Ile Lys
65 70 75
<210> 73
<211> 383
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(381)
<400> 73
ttg ctc tat agt gaa atc att gtc gca ggg cga gtg gcg cgc aat gag 48
Leu Leu Tyr Ser Glu Ile Ile Val Ala Gly Arg Val Ala Arg Asn Glu
1 5 10 15
ttg ttt aaa ttc aac cgc ttg cac acc aaa atc tct att tta caa gat 96
Leu Phe Lys Phe Asn Arg Leu His Thr Lys Ile Ser Ile Leu Gln Asp
20 25 30
gag aaa ccc atc tat tat gac aac acg att tta gat ccc aaa acc acc 144
Glu Lys Pro Ile Tyr Tyr Asp Asn Thr Ile Leu Asp Pro Lys Thr Thr
35 40 45
gac tta aat aac atg tgc atg ttt gat ggc tat acg cat tat ttg aat 192
Asp Leu Asn Asn Met Cys Met Phe Asp Gly Tyr Thr His Tyr Leu Asn
50 55 60
ttg gtg ctt gtc aat tgc ccc ata gag ctc tct ggt gtg cga gaa tgc 240
Leu Val Leu Val Asn Cys Pro Ile Glu Leu Ser Gly Val Arg Glu Cys
65 70 75 80
att gaa gaa agc gaa ggg gtg gat ggg gca gtg agt gaa acc gct agt 288
Ile Glu Glu Ser Glu Gly Val Asp Gly Ala Val Ser Glu Thr Ala Ser
85 90 95
tct cat tta tgc gtg aaa gct tta gcg aaa ggc tca gaa ccc tta ttg 336
Ser His Leu Cys Val Lys Ala Leu Ala Lys Gly Ser Glu Pro Leu Leu
100 105 110
cat tta aga gaa aaa atc gct cgc ttg gtt acg caa acc acc acg ca 383
His Leu Arg Glu Lys Ile Ala Arg Leu Val Thr Gln Thr Thr Thr
115 120 125
<210> 74
<211> 127
<212> PRT
<213> Helicobacter pylori
<400> 74
Leu Leu Tyr Ser Glu Ile Ile Val Ala Gly Arg Val Ala Arg Asn Glu
1 5 10 15
Leu Phe Lys Phe Asn Arg Leu His Thr Lys Ile Ser Ile Leu Gln Asp
20 25 30
Glu Lys Pro Ile Tyr Tyr Asp Asn Thr Ile Leu Asp Pro Lys Thr Thr
35 40 45
Asp Leu Asn Asn Met Cys Met Phe Asp Gly Tyr Thr His Tyr Leu Asn
50 55 60
Leu Val Leu Val Asn Cys Pro Ile Glu Leu Ser Gly Val Arg Glu Cys
65 70 75 80
Ile Glu Glu Ser Glu Gly Val Asp Gly Ala Val Ser Glu Thr Ala Ser
85 90 95
Ser His Leu Cys Val Lys Ala Leu Ala Lys Gly Ser Glu Pro Leu Leu

```
          100                 105                 110
His Leu Arg Glu Lys Ile Ala Arg Leu Val Thr Gln Thr Thr Thr
        115                 120                 125
<210> 75
<211> 165
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(165)
<400> 75
aaa gaa ttg tta aac aac cac ttc aaa caa cgc ctg gcc ttt agg tgt   48
Lys Glu Leu Leu Asn Asn His Phe Lys Gln Arg Leu Ala Phe Arg Cys
  1               5                  10                  15
aat ggt gag aac ttg agc gct atc aaa aaa gat tta cct cta tta aca   96
Asn Gly Glu Asn Leu Ser Ala Ile Lys Lys Asp Leu Pro Leu Leu Thr
             20                  25                  30
aac gaa ctc aac gcg cta ttt gta gag ctt tct aaa gac agc cat act   144
Asn Glu Leu Asn Ala Leu Phe Val Glu Leu Ser Lys Asp Ser His Thr
         35                  40                  45
gaa ttc agg cct ttc agc tta                                     165
Glu Phe Arg Pro Phe Ser Leu
     50                  55
<210> 76
<211> 55
<212> PRT
<213> Helicobacter pylori
<400> 76
Lys Glu Leu Leu Asn Asn His Phe Lys Gln Arg Leu Ala Phe Arg Cys
  1               5                  10                  15
Asn Gly Glu Asn Leu Ser Ala Ile Lys Lys Asp Leu Pro Leu Leu Thr
             20                  25                  30
Asn Glu Leu Asn Ala Leu Phe Val Glu Leu Ser Lys Asp Ser His Thr
         35                  40                  45
Glu Phe Arg Pro Phe Ser Leu
     50                  55
<210> 77
<211> 854
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(852)
<400> 77
act tct tta aac aag ctc att tac aca ggg caa atc att cct gat agg   48
Thr Ser Leu Asn Lys Leu Ile Tyr Thr Gly Gln Ile Ile Pro Asp Arg
  1               5                  10                  15
ggt tcg tgg ttg tat ttt gaa tac gat tct aaa gat gtt tta tac gct   96
Gly Ser Trp Leu Tyr Phe Glu Tyr Asp Ser Lys Asp Val Leu Tyr Ala
             20                  25                  30
cgt atc aat aaa cgc cgt aaa gtg cct gtt acc att tta ttc agg gcg   144
Arg Ile Asn Lys Arg Arg Lys Val Pro Val Thr Ile Leu Phe Arg Ala
         35                  40                  45
atg gat tat caa aaa caa gac atc atc aaa atg ttc tac ccg ctt gtt   192
Met Asp Tyr Gln Lys Gln Asp Ile Ile Lys Met Phe Tyr Pro Leu Val
     50                  55                  60
aaa gtg cgt tat gaa aac gat aaa tat ttg atc ccg ttt gct tca tta   240
Lys Val Arg Tyr Glu Asn Asp Lys Tyr Leu Ile Pro Phe Ala Ser Leu
 65                  70                  75                  80
gac gcc aat caa aga atg gaa ttt gac ttg aaa gat cct caa ggc aag   288
Asp Ala Asn Gln Arg Met Glu Phe Asp Leu Lys Asp Pro Gln Gly Lys
```

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                85                  90                  95
gtt att ctt tta gcg ggt aaa aag ctc act tca aga aag att aaa gag   336
Val Ile Leu Leu Ala Gly Lys Lys Leu Thr Ser Arg Lys Ile Lys Glu
            100                 105                 110
ctt aaa gaa aac cat tta gaa tgg gtg gaa tac cct atg gat att tta   384
Leu Lys Glu Asn His Leu Glu Trp Val Glu Tyr Pro Met Asp Ile Leu
        115                 120                 125
ctc aat cgc cat tta gct gag cct gtt atg gta ggg aaa gaa gtc tta   432
Leu Asn Arg His Leu Ala Glu Pro Val Met Val Gly Lys Glu Val Leu
    130                 135                 140
ttg gac atg ctc act cag cta gat aaa aac aaa tta gaa aaa atc cac   480
Leu Asp Met Leu Thr Gln Leu Asp Lys Asn Lys Leu Glu Lys Ile His
145                 150                 155                 160
gat tta ggc gtg caa gaa ttt gtg atc atc aac gat ctg gcg tta ggg   528
Asp Leu Gly Val Gln Glu Phe Val Ile Ile Asn Asp Leu Ala Leu Gly
                165                 170                 175
cat gac gct tcc att atc caa tct ttt tca gcc gat tct gag tct ttg   576
His Asp Ala Ser Ile Ile Gln Ser Phe Ser Ala Asp Ser Glu Ser Leu
            180                 185                 190
aaa tta ctc aag caa acc gaa aaa att gat gat gaa aac gct cta gcg   624
Lys Leu Leu Lys Gln Thr Glu Lys Ile Asp Asp Glu Asn Ala Leu Ala
        195                 200                 205
gcg att cgt atc cat aag gtt atg aaa cca ggc gat ccc gtt acg act   672
Ala Ile Arg Ile His Lys Val Met Lys Pro Gly Asp Pro Val Thr Thr
    210                 215                 220
gaa gtg gct aag cag ttt gtc aaa aaa ctt ttc ttt gat cca gaa cgc   720
Glu Val Ala Lys Gln Phe Val Lys Lys Leu Phe Phe Asp Pro Glu Arg
225                 230                 235                 240
tat gat ttg acc atg gtg ggc cgc atg aaa atg aat cac aag tta ggc   768
Tyr Asp Leu Thr Met Val Gly Arg Met Lys Met Asn His Lys Leu Gly
                245                 250                 255
ttg cat gtg cct gat tac att acg act tta acg cat gaa gat att atc   816
Leu His Val Pro Asp Tyr Ile Thr Thr Leu Thr His Glu Asp Ile Ile
            260                 265                 270
acc acc gtt aaa tac ctc atg aag atc aaa aac aat ca                854
Thr Thr Val Lys Tyr Leu Met Lys Ile Lys Asn Asn
        275                 280
<210> 78
<211> 284
<212> PRT
<213> Helicobacter pylori
<400> 78
Thr Ser Leu Asn Lys Leu Ile Tyr Thr Gly Gln Ile Ile Pro Asp Arg
  1               5                  10                  15
Gly Ser Trp Leu Tyr Phe Glu Tyr Asp Ser Lys Asp Val Leu Tyr Ala
            20                  25                  30
Arg Ile Asn Lys Arg Arg Lys Val Pro Val Thr Ile Leu Phe Arg Ala
        35                  40                  45
Met Asp Tyr Gln Lys Gln Asp Ile Ile Lys Met Phe Tyr Pro Leu Val
    50                  55                  60
Lys Val Arg Tyr Glu Asn Asp Lys Tyr Leu Ile Pro Phe Ala Ser Leu
65                  70                  75                  80
Asp Ala Asn Gln Arg Met Glu Phe Asp Leu Lys Asp Pro Gln Gly Lys
                85                  90                  95
Val Ile Leu Leu Ala Gly Lys Lys Leu Thr Ser Arg Lys Ile Lys Glu
            100                 105                 110
Leu Lys Glu Asn His Leu Glu Trp Val Glu Tyr Pro Met Asp Ile Leu
        115                 120                 125
Leu Asn Arg His Leu Ala Glu Pro Val Met Val Gly Lys Glu Val Leu
    130                 135                 140
Leu Asp Met Leu Thr Gln Leu Asp Lys Asn Lys Leu Glu Lys Ile His
```

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145                 150                 155                 160
Asp Leu Gly Val Gln Glu Phe Val Ile Ile Asn Asp Leu Ala Leu Gly
                165                 170                 175
His Asp Ala Ser Ile Ile Gln Ser Phe Ser Ala Asp Ser Glu Ser Leu
            180                 185                 190
Lys Leu Leu Lys Gln Thr Glu Lys Ile Asp Asp Glu Asn Ala Leu Ala
        195                 200                 205
Ala Ile Arg Ile His Lys Val Met Lys Pro Gly Asp Pro Val Thr Thr
    210                 215                 220
Glu Val Ala Lys Gln Phe Val Lys Lys Leu Phe Phe Asp Pro Glu Arg
225                 230                 235                 240
Tyr Asp Leu Thr Met Val Gly Arg Met Lys Met Asn His Lys Leu Gly
                245                 250                 255
Leu His Val Pro Asp Tyr Ile Thr Thr Leu Thr His Glu Asp Ile Ile
            260                 265                 270
Thr Thr Val Lys Tyr Leu Met Lys Ile Lys Asn Asn
        275                 280
<210> 79
<211> 1843
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(1842)
<400> 79
aga agc gac gct ccc att gta ggc acg ggg att gaa aaa att att gct   48
Arg Ser Asp Ala Pro Ile Val Gly Thr Gly Ile Glu Lys Ile Ile Ala
  1               5                  10                  15
agg gat tct tgg gga gcg atc aaa gcc aat cgc gca ggc gtt gta gaa   96
Arg Asp Ser Trp Gly Ala Ile Lys Ala Asn Arg Ala Gly Val Val Glu
             20                  25                  30
aaa att gat tct aaa aat att tat att tta ggc gaa agc aaa gaa gaa  144
Lys Ile Asp Ser Lys Asn Ile Tyr Ile Leu Gly Glu Ser Lys Glu Glu
         35                  40                  45
gcc tat att gat gcg tat tct ttg caa aaa aac ttg cgc acc aac caa  192
Ala Tyr Ile Asp Ala Tyr Ser Leu Gln Lys Asn Leu Arg Thr Asn Gln
     50                  55                  60
aac acc agt ttc aat caa gtc cct atc gtt aaa gtg ggc gat aaa gtg  240
Asn Thr Ser Phe Asn Gln Val Pro Ile Val Lys Val Gly Asp Lys Val
 65                  70                  75                  80
gga gcc ggg caa atc atc gct gat ggc cct agc atg gat aga ggc gag  288
Gly Ala Gly Gln Ile Ile Ala Asp Gly Pro Ser Met Asp Arg Gly Glu
                 85                  90                  95
ttg gcg tta ggg aaa aat gtg cgc gtg gcg ttc atg cct tgg aat ggc  336
Leu Ala Leu Gly Lys Asn Val Arg Val Ala Phe Met Pro Trp Asn Gly
            100                 105                 110
tat aac ttt gaa gac gcg atc gtg gtg agt gag tgc atc act aaa gat  384
Tyr Asn Phe Glu Asp Ala Ile Val Val Ser Glu Cys Ile Thr Lys Asp
        115                 120                 125
gat att ttc act tcc acc cac att tat gaa aaa gaa gtg gat gct agg  432
Asp Ile Phe Thr Ser Thr His Ile Tyr Glu Lys Glu Val Asp Ala Arg
    130                 135                 140
gag ctt aag cat ggt gtg gaa gaa ttt acc gct gat att cct gat gtg  480
Glu Leu Lys His Gly Val Glu Glu Phe Thr Ala Asp Ile Pro Asp Val
145                 150                 155                 160
aaa gaa gaa gcg ctc gct cat ctt gat gaa agc ggg atc gtt aaa gtc  528
Lys Glu Glu Ala Leu Ala His Leu Asp Glu Ser Gly Ile Val Lys Val
                165                 170                 175
ggt act tat gtg agc gct ggc atg att ttg gtg ggc aaa act tct cct  576
Gly Thr Tyr Val Ser Ala Gly Met Ile Leu Val Gly Lys Thr Ser Pro
            180                 185                 190
```

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aaa ggc gag att aaa agc acg cct gaa gag cgg ctt tta agg gct att   624
Lys Gly Glu Ile Lys Ser Thr Pro Glu Glu Arg Leu Leu Arg Ala Ile
        195                 200                 205
ttt ggg gat aaa gcc ggg cat gtg gtc aat aag agt ttg tat tgc cct   672
Phe Gly Asp Lys Ala Gly His Val Val Asn Lys Ser Leu Tyr Cys Pro
    210                 215                 220
ccc agt ttg gaa ggc acg gtg att gat gtg aaa gtc ttc act aaa aaa   720
Pro Ser Leu Glu Gly Thr Val Ile Asp Val Lys Val Phe Thr Lys Lys
225                 230                 235                 240
ggc tat gag aaa gac gcg cga gtt ttg agc gcg tat gaa gaa gaa aaa   768
Gly Tyr Glu Lys Asp Ala Arg Val Leu Ser Ala Tyr Glu Glu Glu Lys
                245                 250                 255
gcc aag ctt gat atg gag cat ttt gat cgc ttg acc atg ctc aat aga   816
Ala Lys Leu Asp Met Glu His Phe Asp Arg Leu Thr Met Leu Asn Arg
            260                 265                 270
gaa gaa ttg ttg cgc gtt agc tcg ctc ctt tct caa gcg att tta gaa   864
Glu Glu Leu Leu Arg Val Ser Ser Leu Leu Ser Gln Ala Ile Leu Glu
        275                 280                 285
gag cct ttc agc cat aac ggc aag gat tat aaa gaa ggc gat caa atc   912
Glu Pro Phe Ser His Asn Gly Lys Asp Tyr Lys Glu Gly Asp Gln Ile
    290                 295                 300
cct aaa gaa gaa atc gct tca atc aac cgc ttc act ttg gct agt ttg   960
Pro Lys Glu Glu Ile Ala Ser Ile Asn Arg Phe Thr Leu Ala Ser Leu
305                 310                 315                 320
gtc aaa aag tat tct aaa gaa gtg caa aac cac tat gaa atc act aaa  1008
Val Lys Lys Tyr Ser Lys Glu Val Gln Asn His Tyr Glu Ile Thr Lys
                325                 330                 335
aac aat ttc tta gag caa aag aaa gtt ttg ggc gaa gag cat gaa gaa  1056
Asn Asn Phe Leu Glu Gln Lys Lys Val Leu Gly Glu Glu His Glu Glu
            340                 345                 350
aag ctt tct att tta gaa aaa gat gat att ttg cct aat ggc gtg atc  1104
Lys Leu Ser Ile Leu Glu Lys Asp Asp Ile Leu Pro Asn Gly Val Ile
        355                 360                 365
aaa aaa gtc aag ctc tat atc gct aca aaa cga aag ctt aaa gtg ggc  1152
Lys Lys Val Lys Leu Tyr Ile Ala Thr Lys Arg Lys Leu Lys Val Gly
    370                 375                 380
gat aaa atg gca gga agg cat ggg aat aaa ggg att gtg tct aat atc  1200
Asp Lys Met Ala Gly Arg His Gly Asn Lys Gly Ile Val Ser Asn Ile
385                 390                 395                 400
gtg ccg gtt gcg gat atg cct tat acc gct gat ggc gag cct gta gat  1248
Val Pro Val Ala Asp Met Pro Tyr Thr Ala Asp Gly Glu Pro Val Asp
                405                 410                 415
att gtt tta aac cct tta ggc gtg cca agc cgc atg aat atc ggg cag  1296
Ile Val Leu Asn Pro Leu Gly Val Pro Ser Arg Met Asn Ile Gly Gln
            420                 425                 430
att tta gaa atg cat tta ggc tta gtg ggg aaa gaa ttt ggg aag caa  1344
Ile Leu Glu Met His Leu Gly Leu Val Gly Lys Glu Phe Gly Lys Gln
        435                 440                 445
atc gct cgc atg cta gag gat aaa acc aaa gat ttt gcc aaa gaa ttg  1392
Ile Ala Arg Met Leu Glu Asp Lys Thr Lys Asp Phe Ala Lys Glu Leu
    450                 455                 460
cgt gct aaa atg cta gaa atc gct aac gct att aat gaa aaa gac ccc  1440
Arg Ala Lys Met Leu Glu Ile Ala Asn Ala Ile Asn Glu Lys Asp Pro
465                 470                 475                 480
ttg aca atc cat gcg ctt gag aat tgt tct gat gaa gag ctt ttg gaa  1488
Leu Thr Ile His Ala Leu Glu Asn Cys Ser Asp Glu Glu Leu Leu Glu
                485                 490                 495
tac gca aaa gat tgg agc aag ggc gtt aag atg gct atc cct gtg ttt  1536
Tyr Ala Lys Asp Trp Ser Lys Gly Val Lys Met Ala Ile Pro Val Phe
            500                 505                 510
gaa ggc atc tcg caa gaa aaa ttt tat aag cta ttt gaa tta gct aag  1584
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Glu Gly Ile Ser Gln Glu Lys Phe Tyr Lys Leu Phe Glu Leu Ala Lys
        515                 520                 525
atc gct atg gat ggc aaa atg gat ctg tat gac gga cgc aca ggc gag   1632
Ile Ala Met Asp Gly Lys Met Asp Leu Tyr Asp Gly Arg Thr Gly Glu
    530                 535                 540
aaa atg agg gag cgc gtg aat gtg ggc tac atg tat atg atc aaa ctc   1680
Lys Met Arg Glu Arg Val Asn Val Gly Tyr Met Tyr Met Ile Lys Leu
545                 550                 555                 560
cac cat tta gtg gat gaa aaa gtc cat gcc aga agc aca ggc cct tat   1728
His His Leu Val Asp Glu Lys Val His Ala Arg Ser Thr Gly Pro Tyr
                565                 570                 575
agc tta gta acg cac cag ccc gtg ggg ggt aaa gcg ctc ttt ggg ggt   1776
Ser Leu Val Thr His Gln Pro Val Gly Gly Lys Ala Leu Phe Gly Gly
            580                 585                 590
caa agg ttt ggg gaa atg gaa gtg tgg gcc ttg gaa gct tat ggc gca   1824
Gln Arg Phe Gly Glu Met Glu Val Trp Ala Leu Glu Ala Tyr Gly Ala
        595                 600                 605
gcg cac act cta aaa gaa a                                        1843
Ala His Thr Leu Lys Glu
    610
<210> 80
<211> 614
<212> PRT
<213> Helicobacter pylori
<400> 80
Arg Ser Asp Ala Pro Ile Val Gly Thr Gly Ile Glu Lys Ile Ile Ala
  1               5                  10                  15
Arg Asp Ser Trp Gly Ala Ile Lys Ala Asn Arg Ala Gly Val Val Glu
            20                  25                  30
Lys Ile Asp Ser Lys Asn Ile Tyr Ile Leu Gly Glu Ser Lys Glu Glu
        35                  40                  45
Ala Tyr Ile Asp Ala Tyr Ser Leu Gln Lys Asn Leu Arg Thr Asn Gln
    50                  55                  60
Asn Thr Ser Phe Asn Gln Val Pro Ile Val Lys Val Gly Asp Lys Val
65                  70                  75                  80
Gly Ala Gly Gln Ile Ile Ala Asp Gly Pro Ser Met Asp Arg Gly Glu
                85                  90                  95
Leu Ala Leu Gly Lys Asn Val Arg Val Ala Phe Met Pro Trp Asn Gly
            100                 105                 110
Tyr Asn Phe Glu Asp Ala Ile Val Val Ser Glu Cys Ile Thr Lys Asp
        115                 120                 125
Asp Ile Phe Thr Ser Thr His Ile Tyr Glu Lys Glu Val Asp Ala Arg
    130                 135                 140
Glu Leu Lys His Gly Val Glu Glu Phe Thr Ala Asp Ile Pro Asp Val
145                 150                 155                 160
Lys Glu Glu Ala Leu Ala His Leu Asp Glu Ser Gly Ile Val Lys Val
                165                 170                 175
Gly Thr Tyr Val Ser Ala Gly Met Ile Leu Val Gly Lys Thr Ser Pro
            180                 185                 190
Lys Gly Glu Ile Lys Ser Thr Pro Glu Glu Arg Leu Leu Arg Ala Ile
        195                 200                 205
Phe Gly Asp Lys Ala Gly His Val Val Asn Lys Ser Leu Tyr Cys Pro
    210                 215                 220
Pro Ser Leu Glu Gly Thr Val Ile Asp Val Lys Val Phe Thr Lys Lys
225                 230                 235                 240
Gly Tyr Glu Lys Asp Ala Arg Val Leu Ser Ala Tyr Glu Glu Glu Lys
                245                 250                 255
Ala Lys Leu Asp Met Glu His Phe Asp Arg Leu Thr Met Leu Asn Arg
            260                 265                 270
Glu Glu Leu Leu Arg Val Ser Ser Leu Leu Ser Gln Ala Ile Leu Glu
        275                 280                 285
```

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Glu Pro Phe Ser His Asn Gly Lys Asp Tyr Lys Glu Gly Asp Gln Ile
    290                 295                 300
Pro Lys Glu Glu Ile Ala Ser Ile Asn Arg Phe Thr Leu Ala Ser Leu
305                 310                 315                 320
Val Lys Lys Tyr Ser Lys Glu Val Gln Asn His Tyr Glu Ile Thr Lys
                325                 330                 335
Asn Asn Phe Leu Glu Gln Lys Lys Val Leu Gly Glu Glu His Glu Glu
            340                 345                 350
Lys Leu Ser Ile Leu Glu Lys Asp Asp Ile Leu Pro Asn Gly Val Ile
        355                 360                 365
Lys Lys Val Lys Leu Tyr Ile Ala Thr Lys Arg Lys Leu Lys Val Gly
    370                 375                 380
Asp Lys Met Ala Gly Arg His Gly Asn Lys Gly Ile Val Ser Asn Ile
385                 390                 395                 400
Val Pro Val Ala Asp Met Pro Tyr Thr Ala Asp Gly Glu Pro Val Asp
                405                 410                 415
Ile Val Leu Asn Pro Leu Gly Val Pro Ser Arg Met Asn Ile Gly Gln
            420                 425                 430
Ile Leu Glu Met His Leu Gly Leu Val Gly Lys Glu Phe Gly Lys Gln
        435                 440                 445
Ile Ala Arg Met Leu Glu Asp Lys Thr Lys Asp Phe Ala Lys Glu Leu
    450                 455                 460
Arg Ala Lys Met Leu Glu Ile Ala Asn Ala Ile Asn Glu Lys Asp Pro
465                 470                 475                 480
Leu Thr Ile His Ala Leu Glu Asn Cys Ser Asp Glu Glu Leu Leu Glu
                485                 490                 495
Tyr Ala Lys Asp Trp Ser Lys Gly Val Lys Met Ala Ile Pro Val Phe
            500                 505                 510
Glu Gly Ile Ser Gln Glu Lys Phe Tyr Lys Leu Phe Glu Leu Ala Lys
        515                 520                 525
Ile Ala Met Asp Gly Lys Met Asp Leu Tyr Asp Gly Arg Thr Gly Glu
    530                 535                 540
Lys Met Arg Glu Arg Val Asn Val Gly Tyr Met Tyr Met Ile Lys Leu
545                 550                 555                 560
His His Leu Val Asp Glu Lys Val His Ala Arg Ser Thr Gly Pro Tyr
                565                 570                 575
Ser Leu Val Thr His Gln Pro Val Gly Gly Lys Ala Leu Phe Gly Gly
            580                 585                 590
Gln Arg Phe Gly Glu Met Glu Val Trp Ala Leu Glu Ala Tyr Gly Ala
        595                 600                 605
Ala His Thr Leu Lys Glu
    610
<210> 81
<211> 1040
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(1038)
<400> 81
ata aaa atg att gat gtg aat ggt tta tta aaa gaa ctg gat gat gcc   48
Ile Lys Met Ile Asp Val Asn Gly Leu Leu Lys Glu Leu Asp Asp Ala
 1               5                  10                  15
tta gat aaa gtt gtt gct aaa aaa gag cca gag agt ttt ctc aag ccg   96
Leu Asp Lys Val Val Ala Lys Lys Glu Pro Glu Ser Phe Leu Lys Pro
            20                  25                  30
atc atc tca cca ata gag gac tac caa aag agt gtc agg caa att caa  144
Ile Ile Ser Pro Ile Glu Asp Tyr Gln Lys Ser Val Arg Gln Ile Gln
        35                  40                  45
gcg caa ttc aca gac gcg cca aag ttc aat gaa gag ggc gct tac cca  192
Ala Gln Phe Thr Asp Ala Pro Lys Phe Asn Glu Glu Gly Ala Tyr Pro
```

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     50                  55                  60
caa ttt tta agc tgt ggt tta ttg gaa att aaa ggc aag aat ggc gct   240
Gln Phe Leu Ser Cys Gly Leu Leu Glu Ile Lys Gly Lys Asn Gly Ala
 65                  70                  75                  80
agc atg gaa ttt tgc ttg cct aaa gtt tat cct ttc ccc cct aaa agc   288
Ser Met Glu Phe Cys Leu Pro Lys Val Tyr Pro Phe Pro Pro Lys Ser
                 85                  90                  95
ttg tat ata gag cat gaa aaa gac ggg cag ttt tta aga gaa atg ctc   336
Leu Tyr Ile Glu His Glu Lys Asp Gly Gln Phe Leu Arg Glu Met Leu
            100                 105                 110
atg cgc ttg cta tcc agt gcg cct tta gtg caa tta gaa gtg atc tta   384
Met Arg Leu Leu Ser Ser Ala Pro Leu Val Gln Leu Glu Val Ile Leu
        115                 120                 125
gtt gat gcg ctg agc cta ggg ggc att ttc aat ctg gca aga agg ctt   432
Val Asp Ala Leu Ser Leu Gly Gly Ile Phe Asn Leu Ala Arg Arg Leu
    130                 135                 140
tta cat aaa gac aat gac ttt att tac cag caa agg att tta act gaa   480
Leu His Lys Asp Asn Asp Phe Ile Tyr Gln Gln Arg Ile Leu Thr Glu
145                 150                 155                 160
agc aag gaa ata gaa gaa gcc cta aag cat ttg tat gaa tat tta aag   528
Ser Lys Glu Ile Glu Glu Ala Leu Lys His Leu Tyr Glu Tyr Leu Lys
                165                 170                 175
gtt aat ttg caa gaa aaa tta gcc ggt tat aaa gat ttt gcg cat tat   576
Val Asn Leu Gln Glu Lys Leu Ala Gly Tyr Lys Asp Phe Ala His Tyr
            180                 185                 190
aat gaa gaa aaa aaa gac cgc ttg cct tta aaa gcg ctt ttt tta agc   624
Asn Glu Glu Lys Lys Asp Arg Leu Pro Leu Lys Ala Leu Phe Leu Ser
        195                 200                 205
ggt gta gat gct tta agt caa aac gcg ctt tat tat ctg gaa aaa atc   672
Gly Val Asp Ala Leu Ser Gln Asn Ala Leu Tyr Tyr Leu Glu Lys Ile
    210                 215                 220
atg cgt ttt ggc tct aaa aat ggg gtt ttg agc ttt gtc aat ttg gag   720
Met Arg Phe Gly Ser Lys Asn Gly Val Leu Ser Phe Val Asn Leu Glu
225                 230                 235                 240
agt gaa aaa aat aat aaa tcc aca gaa gat ttg aaa cgc tat gcg gag   768
Ser Glu Lys Asn Asn Lys Ser Thr Glu Asp Leu Lys Arg Tyr Ala Glu
                245                 250                 255
tgt ttt aaa gac agg aca agt ttt gaa cgc tta aaa tat ctt aat ata   816
Cys Phe Lys Asp Arg Thr Ser Phe Glu Arg Leu Lys Tyr Leu Asn Ile
            260                 265                 270
gaa gtg atc aat gat cat ggt atc caa tct aag cac atg aaa gac ttc   864
Glu Val Ile Asn Asp His Gly Ile Gln Ser Lys His Met Lys Asp Phe
        275                 280                 285
gct gat aaa att aaa gcg tat tac gag aaa aag aaa gca gtt aaa agg   912
Ala Asp Lys Ile Lys Ala Tyr Tyr Glu Lys Lys Lys Ala Val Lys Arg
    290                 295                 300
gag ttg aaa gac tta caa aaa gac gaa aaa ttt tgg act gaa agc tct   960
Glu Leu Lys Asp Leu Gln Lys Asp Glu Lys Phe Trp Thr Glu Ser Ser
305                 310                 315                 320
cag ttt aaa gtg tct gtg ccg gtg ggg tgg gat att aac cat aag gaa  1008
Gln Phe Lys Val Ser Val Pro Val Gly Trp Asp Ile Asn His Lys Glu
                325                 330                 335
gtg tgt ttt gaa atc ggt aac gaa caa aac ca                      1040
Val Cys Phe Glu Ile Gly Asn Glu Gln Asn
            340                 345
```

<210> 82
<211> 346
<212> PRT
<213> Helicobacter pylori
<400> 82
Ile Lys Met Ile Asp Val Asn Gly Leu Leu Lys Glu Leu Asp Asp Ala

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 1               5                  10                  15
Leu Asp Lys Val Val Ala Lys Lys Glu Pro Glu Ser Phe Leu Lys Pro
            20                  25                  30
Ile Ile Ser Pro Ile Glu Asp Tyr Gln Lys Ser Val Arg Gln Ile Gln
        35                  40                  45
Ala Gln Phe Thr Asp Ala Pro Lys Phe Asn Glu Glu Gly Ala Tyr Pro
    50                  55                  60
Gln Phe Leu Ser Cys Gly Leu Leu Glu Ile Lys Gly Lys Asn Gly Ala
65                  70                  75                  80
Ser Met Glu Phe Cys Leu Pro Lys Val Tyr Pro Phe Pro Pro Lys Ser
                85                  90                  95
Leu Tyr Ile Glu His Glu Lys Asp Gly Gln Phe Leu Arg Glu Met Leu
            100                 105                 110
Met Arg Leu Leu Ser Ser Ala Pro Leu Val Gln Leu Glu Val Ile Leu
        115                 120                 125
Val Asp Ala Leu Ser Leu Gly Gly Ile Phe Asn Leu Ala Arg Arg Leu
    130                 135                 140
Leu His Lys Asp Asn Asp Phe Ile Tyr Gln Gln Arg Ile Leu Thr Glu
145                 150                 155                 160
Ser Lys Glu Ile Glu Glu Ala Leu Lys His Leu Tyr Glu Tyr Leu Lys
                165                 170                 175
Val Asn Leu Gln Glu Lys Leu Ala Gly Tyr Lys Asp Phe Ala His Tyr
            180                 185                 190
Asn Glu Glu Lys Lys Asp Arg Leu Pro Leu Lys Ala Leu Phe Leu Ser
        195                 200                 205
Gly Val Asp Ala Leu Ser Gln Asn Ala Leu Tyr Tyr Leu Glu Lys Ile
    210                 215                 220
Met Arg Phe Gly Ser Lys Asn Gly Val Leu Ser Phe Val Asn Leu Glu
225                 230                 235                 240
Ser Glu Lys Asn Asn Lys Ser Thr Glu Asp Leu Lys Arg Tyr Ala Glu
                245                 250                 255
Cys Phe Lys Asp Arg Thr Ser Phe Glu Arg Leu Lys Tyr Leu Asn Ile
            260                 265                 270
Glu Val Ile Asn Asp His Gly Ile Gln Ser Lys His Met Lys Asp Phe
        275                 280                 285
Ala Asp Lys Ile Lys Ala Tyr Tyr Glu Lys Lys Lys Ala Val Lys Arg
    290                 295                 300
Glu Leu Lys Asp Leu Gln Lys Asp Glu Lys Phe Trp Thr Glu Ser Ser
305                 310                 315                 320
Gln Phe Lys Val Ser Val Pro Val Gly Trp Asp Ile Asn His Lys Glu
                325                 330                 335
Val Cys Phe Glu Ile Gly Asn Glu Gln Asn
            340                 345
```

<210> 83
<211> 63
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(63)
<400> 83

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ata aaa ccc acc gaa caa aaa ggt ttt ttt aaa agt ttc ctt gat aag   48
Ile Lys Pro Thr Glu Gln Lys Gly Phe Phe Lys Ser Phe Leu Asp Lys
 1               5                  10                  15
att tct aaa ttc ttt                                              63
Ile Ser Lys Phe Phe
            20
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<210> 84
<211> 21
<212> PRT
<213> Helicobacter pylori

<400> 84
Ile Lys Pro Thr Glu Gln Lys Gly Phe Phe Lys Ser Phe Leu Asp Lys
1 5 10 15
Ile Ser Lys Phe Phe
20

<210> 85
<211> 846
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(846)
<400> 85

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gtg ttc aaa gac agc aaa aaa gac gct tgc ggg ttc atc tat gag atc   48
Val Phe Lys Asp Ser Lys Lys Asp Ala Cys Gly Phe Ile Tyr Glu Ile
 1               5                  10                  15
agc gag ttc atg aaa gcc tat acc gca ttg cta aaa aaa caa gac cga   96
Ser Glu Phe Met Lys Ala Tyr Thr Ala Leu Leu Lys Lys Gln Asp Arg
            20                  25                  30
tac gtc tat tta ttg agg tat ctc ccc tct agg tat tgg gcc agc att  144
Tyr Val Tyr Leu Leu Arg Tyr Leu Pro Ser Arg Tyr Trp Ala Ser Ile
        35                  40                  45
tta acg act gcc ctt tat gtc aaa tac cct gat ttt gac gct ttg aaa  192
Leu Thr Thr Ala Leu Tyr Val Lys Tyr Pro Asp Phe Asp Ala Leu Lys
    50                  55                  60
aag ctt ttg gtg tct tat tat tac caa act tgg att gca gga ggc acg  240
Lys Leu Leu Val Ser Tyr Tyr Tyr Gln Thr Trp Ile Ala Gly Gly Thr
65                  70                  75                  80
atc acg cgc atc aag caa acc agt atc aac att atc aaa aac gtt aaa  288
Ile Thr Arg Ile Lys Gln Thr Ser Ile Asn Ile Ile Lys Asn Val Lys
                85                  90                  95
agc aat aag agc gtt gaa acc atc aaa gag ctt ata ttg aat agc atc  336
Ser Asn Lys Ser Val Glu Thr Ile Lys Glu Leu Ile Leu Asn Ser Ile
            100                 105                 110
gac tct tat aac acc ttt gat caa tac ctc tat aac tta tgg gat agc  384
Asp Ser Tyr Asn Thr Phe Asp Gln Tyr Leu Tyr Asn Leu Trp Asp Ser
        115                 120                 125
tct tct gtt tat cat agc aaa tgg gtg cgt cct gtc tta gcc cta gct  432
Ser Ser Val Tyr His Ser Lys Trp Val Arg Pro Val Leu Ala Leu Ala
    130                 135                 140
aat tat ttc atg gca gat gaa gag aaa ccc cat ttt atc gct atg gat  480
Asn Tyr Phe Met Ala Asp Glu Glu Lys Pro His Phe Ile Ala Met Asp
145                 150                 155                 160
gcc gaa acc caa gtg gag cat att ttg cca caa acg ccc aaa aga ggc  528
Ala Glu Thr Gln Val Glu His Ile Leu Pro Gln Thr Pro Lys Arg Gly
                165                 170                 175
agt caa tgg aac gcg gat ttt gac aaa gaa aaa aga gaa gaa tgg gta  576
Ser Gln Trp Asn Ala Asp Phe Asp Lys Glu Lys Arg Glu Glu Trp Val
            180                 185                 190
aat aat atc gcg aat tta acc ctt tta aag cgt aaa aag aac gcg cat  624
Asn Asn Ile Ala Asn Leu Thr Leu Leu Lys Arg Lys Lys Asn Ala His
        195                 200                 205
gct tta aac ggg gat ttt gat gaa aaa aga aaa att tat gga ggc aaa  672
Ala Leu Asn Gly Asp Phe Asp Glu Lys Arg Lys Ile Tyr Gly Gly Lys
    210                 215                 220
gac acg agc aaa gtg att agc tgt tat gac atc act aaa gaa ttg tat  720
Asp Thr Ser Lys Val Ile Ser Cys Tyr Asp Ile Thr Lys Glu Leu Tyr
225                 230                 235                 240
agc aat tat agg aag tgg aat gag aag tcc ctc caa gag cga tac aaa  768
Ser Asn Tyr Arg Lys Trp Asn Glu Lys Ser Leu Gln Glu Arg Tyr Lys
                245                 250                 255
```

```
tct ttg tat aac act atc acg cct gtt tta cac ata gag ggg caa gaa   816
Ser Leu Tyr Asn Thr Ile Thr Pro Val Leu His Ile Glu Gly Gln Glu
            260                 265                 270
gat gat ttt gaa gat gat ttt gat cta gaa                          846
Asp Asp Phe Glu Asp Asp Phe Asp Leu Glu
        275                 280
<210> 86
<211> 282
<212> PRT
<213> Helicobacter pylori
<400> 86
Val Phe Lys Asp Ser Lys Lys Asp Ala Cys Gly Phe Ile Tyr Glu Ile
  1               5                  10                  15
Ser Glu Phe Met Lys Ala Tyr Thr Ala Leu Leu Lys Lys Gln Asp Arg
             20                  25                  30
Tyr Val Tyr Leu Leu Arg Tyr Leu Pro Ser Arg Tyr Trp Ala Ser Ile
         35                  40                  45
Leu Thr Thr Ala Leu Tyr Val Lys Tyr Pro Asp Phe Asp Ala Leu Lys
     50                  55                  60
Lys Leu Leu Val Ser Tyr Tyr Tyr Gln Thr Trp Ile Ala Gly Gly Thr
 65                  70                  75                  80
Ile Thr Arg Ile Lys Gln Thr Ser Ile Asn Ile Ile Lys Asn Val Lys
                 85                  90                  95
Ser Asn Lys Ser Val Glu Thr Ile Lys Glu Leu Ile Leu Asn Ser Ile
            100                 105                 110
Asp Ser Tyr Asn Thr Phe Asp Gln Tyr Leu Tyr Asn Leu Trp Asp Ser
        115                 120                 125
Ser Ser Val Tyr His Ser Lys Trp Val Arg Pro Val Leu Ala Leu Ala
    130                 135                 140
Asn Tyr Phe Met Ala Asp Glu Glu Lys Pro His Phe Ile Ala Met Asp
145                 150                 155                 160
Ala Glu Thr Gln Val Glu His Ile Leu Pro Gln Thr Pro Lys Arg Gly
                165                 170                 175
Ser Gln Trp Asn Ala Asp Phe Asp Lys Glu Lys Arg Glu Glu Trp Val
            180                 185                 190
Asn Asn Ile Ala Asn Leu Thr Leu Leu Lys Arg Lys Lys Asn Ala His
        195                 200                 205
Ala Leu Asn Gly Asp Phe Asp Glu Lys Arg Lys Ile Tyr Gly Gly Lys
    210                 215                 220
Asp Thr Ser Lys Val Ile Ser Cys Tyr Asp Ile Thr Lys Glu Leu Tyr
225                 230                 235                 240
Ser Asn Tyr Arg Lys Trp Asn Glu Lys Ser Leu Gln Glu Arg Tyr Lys
                245                 250                 255
Ser Leu Tyr Asn Thr Ile Thr Pro Val Leu His Ile Glu Gly Gln Glu
            260                 265                 270
Asp Asp Phe Glu Asp Asp Phe Asp Leu Glu
        275                 280
<210> 87
<211> 334
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(333)
<400> 87
tat ggc gag ttt tta gaa aaa gaa aaa gag ggc ttt atg gta gat gag   48
Tyr Gly Glu Phe Leu Glu Lys Glu Lys Glu Gly Phe Met Val Asp Glu
  1               5                  10                  15
caa aac cct tat ccg gaa gaa gtc cgc ttt aat gag ttg cgt tta gcg   96
Gln Asn Pro Tyr Pro Glu Glu Val Arg Phe Asn Glu Leu Arg Leu Ala
             20                  25                  30
```

```
gaa ttt gag agc gtt ttt agc gcc att gtg cct tta gag gat tta gat   144
Glu Phe Glu Ser Val Phe Ser Ala Ile Val Pro Leu Glu Asp Leu Asp
         35                  40                  45
aaa cct gca tgc gct cat cat gcc cta aag gct tta gaa gcc acg ctt   192
Lys Pro Ala Cys Ala His His Ala Leu Lys Ala Leu Glu Ala Thr Leu
     50                  55                  60
aaa aat agg gat ttg ggc ttt gat gcg aca gaa ttg gaa cag atc gca   240
Lys Asn Arg Asp Leu Gly Phe Asp Ala Thr Glu Leu Glu Gln Ile Ala
 65                  70                  75                  80
aaa ggt ttc att cct aag ggg tat ttg tgg cat ttt gac gcg aat gtt   288
Lys Gly Phe Ile Pro Lys Gly Tyr Leu Trp His Phe Asp Ala Asn Val
                 85                  90                  95
tta ggg aat gtg gcg ttg gtg aga gaa gag tta tta tta ggc gtg a     334
Leu Gly Asn Val Ala Leu Val Arg Glu Glu Leu Leu Leu Gly Val
            100                 105                 110
<210> 88
<211> 111
<212> PRT
<213> Helicobacter pylori
<400> 88
Tyr Gly Glu Phe Leu Glu Lys Glu Lys Glu Gly Phe Met Val Asp Glu
  1               5                  10                  15
Gln Asn Pro Tyr Pro Glu Glu Val Arg Phe Asn Glu Leu Arg Leu Ala
            20                  25                  30
Glu Phe Glu Ser Val Phe Ser Ala Ile Val Pro Leu Glu Asp Leu Asp
         35                  40                  45
Lys Pro Ala Cys Ala His His Ala Leu Lys Ala Leu Glu Ala Thr Leu
     50                  55                  60
Lys Asn Arg Asp Leu Gly Phe Asp Ala Thr Glu Leu Glu Gln Ile Ala
 65                  70                  75                  80
Lys Gly Phe Ile Pro Lys Gly Tyr Leu Trp His Phe Asp Ala Asn Val
                 85                  90                  95
Leu Gly Asn Val Ala Leu Val Arg Glu Glu Leu Leu Leu Gly Val
            100                 105                 110
<210> 89
<211> 1692
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(1692)
<400> 89
tta gtc agc tct tca gaa tac gct aaa aaa ctc aat gcg att gac aag    48
Leu Val Ser Ser Ser Glu Tyr Ala Lys Lys Leu Asn Ala Ile Asp Lys
  1               5                  10                  15
att aaa aaa acc gaa gaa aag caa aaa gtt tta gat gaa gaa tta gaa    96
Ile Lys Lys Thr Glu Glu Lys Gln Lys Val Leu Asp Glu Glu Leu Glu
            20                  25                  30
gat ggc tat gac ttt ttg aaa gaa aag gat ttt tta gag tgg agc aga   144
Asp Gly Tyr Asp Phe Leu Lys Glu Lys Asp Phe Leu Glu Trp Ser Arg
         35                  40                  45
agc gat agc cca gtg cgc atg tat ttg cgc gaa atg ggg gat ata aaa   192
Ser Asp Ser Pro Val Arg Met Tyr Leu Arg Glu Met Gly Asp Ile Lys
     50                  55                  60
ctt tta agc aaa gat gaa gag att gaa ttg agc aag caa atc cgc ttg   240
Leu Leu Ser Lys Asp Glu Glu Ile Glu Leu Ser Lys Gln Ile Arg Leu
 65                  70                  75                  80
ggt gaa gac att att tta gac gcg atc tgc tcg gtg ccg tat ttg att   288
Gly Glu Asp Ile Ile Leu Asp Ala Ile Cys Ser Val Pro Tyr Leu Ile
                 85                  90                  95
gat ttt atc tat gcg tat aaa gac gct tta atc aat cgt gaa aga agg   336
```

```
Asp Phe Ile Tyr Ala Tyr Lys Asp Ala Leu Ile Asn Arg Glu Arg Arg
                100                 105                 110
gtt aaa gag ctt ttc agg agc ttt gat gat gac gat gaa aat agc gtg   384
Val Lys Glu Leu Phe Arg Ser Phe Asp Asp Asp Asp Glu Asn Ser Val
        115                 120                 125
agc gat tct aaa aaa gat gaa gac aac gaa gaa gat gaa gaa aac gaa   432
Ser Asp Ser Lys Lys Asp Glu Asp Asn Glu Glu Asp Glu Glu Asn Glu
    130                 135                 140
gaa agg aaa aaa gtc gtt tct gaa aaa gac aag aag cgt gta gaa aag   480
Glu Arg Lys Lys Val Val Ser Glu Lys Asp Lys Lys Arg Val Glu Lys
145                 150                 155                 160
gtt caa gaa agc ttt aaa gcc cta gac aag gct aaa aaa gaa tgg ctt   528
Val Gln Glu Ser Phe Lys Ala Leu Asp Lys Ala Lys Lys Glu Trp Leu
                165                 170                 175
aaa gcc ctt gaa gcc ccc ata gat gaa aga gaa gac gaa ttg gtg cgt   576
Lys Ala Leu Glu Ala Pro Ile Asp Glu Arg Glu Asp Glu Leu Val Arg
            180                 185                 190
tca ttg acc cta gct tac aaa cgc caa aca ctc aaa gac aga ctc tat   624
Ser Leu Thr Leu Ala Tyr Lys Arg Gln Thr Leu Lys Asp Arg Leu Tyr
        195                 200                 205
gat tta gaa cct acc agc aaa ctg att aat gaa tta gtc aaa acg atg   672
Asp Leu Glu Pro Thr Ser Lys Leu Ile Asn Glu Leu Val Lys Thr Met
    210                 215                 220
gaa acc act tta aaa agc ggc gat ggg ttt gaa aaa gag ttg aaa cgc   720
Glu Thr Thr Leu Lys Ser Gly Asp Gly Phe Glu Lys Glu Leu Lys Arg
225                 230                 235                 240
ttg gaa tac aaa ctg ccc tta ttc aat gac act ctc atc gca aac cat   768
Leu Glu Tyr Lys Leu Pro Leu Phe Asn Asp Thr Leu Ile Ala Asn His
                245                 250                 255
aaa aaa atc ctt gcc aat atc act aac atg act aaa gaa gat att atc   816
Lys Lys Ile Leu Ala Asn Ile Thr Asn Met Thr Lys Glu Asp Ile Ile
            260                 265                 270
gct caa gtg cca gaa gcg act atg gtg agc gtg tat atg gat ctt aaa   864
Ala Gln Val Pro Glu Ala Thr Met Val Ser Val Tyr Met Asp Leu Lys
        275                 280                 285
aag ctt ttt ttg act aaa gaa gcg agc gaa gaa ggc ttt gat cta gcc   912
Lys Leu Phe Leu Thr Lys Glu Ala Ser Glu Glu Gly Phe Asp Leu Ala
    290                 295                 300
ccc aac aag cta aaa gaa att tta gag caa atc aaa aga ggg aag ttg   960
Pro Asn Lys Leu Lys Glu Ile Leu Glu Gln Ile Lys Arg Gly Lys Leu
305                 310                 315                 320
att tcc gat cgc gct aaa aac aaa atg gct aaa tcc aat tta agg ttg  1008
Ile Ser Asp Arg Ala Lys Asn Lys Met Ala Lys Ser Asn Leu Arg Leu
                325                 330                 335
gtg gtg agc atc gct aaa cga ttc acg agc aga ggc tta cca ttc ttg  1056
Val Val Ser Ile Ala Lys Arg Phe Thr Ser Arg Gly Leu Pro Phe Leu
            340                 345                 350
gat ttg att caa gag ggc aat att ggc ttg atg aaa gcg gtg gat aag  1104
Asp Leu Ile Gln Glu Gly Asn Ile Gly Leu Met Lys Ala Val Asp Lys
        355                 360                 365
ttt gag cat gaa aag ggc ttc aag ttt tct acc tat gcg acc tgg tgg  1152
Phe Glu His Glu Lys Gly Phe Lys Phe Ser Thr Tyr Ala Thr Trp Trp
    370                 375                 380
atc aaa caa gct atc agc aga gcc ata gcc gat cag gcc cgc act atc  1200
Ile Lys Gln Ala Ile Ser Arg Ala Ile Ala Asp Gln Ala Arg Thr Ile
385                 390                 395                 400
cgc atc ccc att cac atg att gat acg att aat cgc atc aat aaa gtc  1248
Arg Ile Pro Ile His Met Ile Asp Thr Ile Asn Arg Ile Asn Lys Val
                405                 410                 415
atg cgc aaa cac att caa gaa aac ggc aaa gag cct gat tta gaa gtg  1296
Met Arg Lys His Ile Gln Glu Asn Gly Lys Glu Pro Asp Leu Glu Val
```

```
            420                 425                 430
gtg gct gaa gaa gtg ggg ctt tcg tta gat aaa gtg aag aat gtg att   1344
Val Ala Glu Glu Val Gly Leu Ser Leu Asp Lys Val Lys Asn Val Ile
        435                 440                 445
aag gtg act aaa gag cct atc agt ttg gaa acc cca gtc ggc aat gat   1392
Lys Val Thr Lys Glu Pro Ile Ser Leu Glu Thr Pro Val Gly Asn Asp
    450                 455                 460
gat gat ggc aag ttt ggg gat ttc gtg gaa gat aag aat atc gtc agc   1440
Asp Asp Gly Lys Phe Gly Asp Phe Val Glu Asp Lys Asn Ile Val Ser
465                 470                 475                 480
tcc att gat cac atc atg cga gaa gat ttg aaa gca caa att gaa agc   1488
Ser Ile Asp His Ile Met Arg Glu Asp Leu Lys Ala Gln Ile Glu Ser
                485                 490                 495
gtt ttg gat cag ttg aat gag cga gaa aaa gcg gtg atc cgc atg cgt   1536
Val Leu Asp Gln Leu Asn Glu Arg Glu Lys Ala Val Ile Arg Met Arg
            500                 505                 510
ttt ggg ctt tta gac gat gaa agc gat cga act tta gaa gaa att ggc   1584
Phe Gly Leu Leu Asp Asp Glu Ser Asp Arg Thr Leu Glu Glu Ile Gly
        515                 520                 525
aag gaa ttg aat gtt act aga gaa agg gtg cgc cag att gaa agc tct   1632
Lys Glu Leu Asn Val Thr Arg Glu Arg Val Arg Gln Ile Glu Ser Ser
    530                 535                 540
gcg att aaa aaa ttg aga agc ccg cag tac ggg cgc att tta aga aac   1680
Ala Ile Lys Lys Leu Arg Ser Pro Gln Tyr Gly Arg Ile Leu Arg Asn
545                 550                 555                 560
tat ttg cgc att                                               1692
Tyr Leu Arg Ile
<210> 90
<211> 564
<212> PRT
<213> Helicobacter pylori
<400> 90
Leu Val Ser Ser Ser Glu Tyr Ala Lys Lys Leu Asn Ala Ile Asp Lys
  1               5                  10                  15
Ile Lys Lys Thr Glu Glu Lys Gln Lys Val Leu Asp Glu Glu Leu Glu
            20                  25                  30
Asp Gly Tyr Asp Phe Leu Lys Glu Lys Asp Phe Leu Glu Trp Ser Arg
        35                  40                  45
Ser Asp Ser Pro Val Arg Met Tyr Leu Arg Glu Met Gly Asp Ile Lys
    50                  55                  60
Leu Leu Ser Lys Asp Glu Glu Ile Glu Leu Ser Lys Gln Ile Arg Leu
65                  70                  75                  80
Gly Glu Asp Ile Ile Leu Asp Ala Ile Cys Ser Val Pro Tyr Leu Ile
                85                  90                  95
Asp Phe Ile Tyr Ala Tyr Lys Asp Ala Leu Ile Asn Arg Glu Arg Arg
            100                 105                 110
Val Lys Glu Leu Phe Arg Ser Phe Asp Asp Asp Asp Glu Asn Ser Val
        115                 120                 125
Ser Asp Ser Lys Lys Asp Glu Asp Asn Glu Glu Asp Glu Glu Asn Glu
    130                 135                 140
Glu Arg Lys Lys Val Val Ser Glu Lys Asp Lys Lys Arg Val Glu Lys
145                 150                 155                 160
Val Gln Glu Ser Phe Lys Ala Leu Asp Lys Ala Lys Lys Glu Trp Leu
                165                 170                 175
Lys Ala Leu Glu Ala Pro Ile Asp Glu Arg Glu Asp Glu Leu Val Arg
            180                 185                 190
Ser Leu Thr Leu Ala Tyr Lys Arg Gln Thr Leu Lys Asp Arg Leu Tyr
        195                 200                 205
Asp Leu Glu Pro Thr Ser Lys Leu Ile Asn Glu Leu Val Lys Thr Met
    210                 215                 220
Glu Thr Thr Leu Lys Ser Gly Asp Gly Phe Glu Lys Glu Leu Lys Arg
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225 230 235 240
Leu Glu Tyr Lys Leu Pro Leu Phe Asn Asp Thr Leu Ile Ala Asn His
245 250 255
Lys Lys Ile Leu Ala Asn Ile Thr Asn Met Thr Lys Glu Asp Ile Ile
260 265 270
Ala Gln Val Pro Glu Ala Thr Met Val Ser Val Tyr Met Asp Leu Lys
275 280 285
Lys Leu Phe Leu Thr Lys Glu Ala Ser Glu Glu Gly Phe Asp Leu Ala
290 295 300
Pro Asn Lys Leu Lys Glu Ile Leu Glu Gln Ile Lys Arg Gly Lys Leu
305 310 315 320
Ile Ser Asp Arg Ala Lys Asn Lys Met Ala Lys Ser Asn Leu Arg Leu
325 330 335
Val Val Ser Ile Ala Lys Arg Phe Thr Ser Arg Gly Leu Pro Phe Leu
340 345 350
Asp Leu Ile Gln Glu Gly Asn Ile Gly Leu Met Lys Ala Val Asp Lys
355 360 365
Phe Glu His Glu Lys Gly Phe Lys Phe Ser Thr Tyr Ala Thr Trp Trp
370 375 380
Ile Lys Gln Ala Ile Ser Arg Ala Ile Ala Asp Gln Ala Arg Thr Ile
385 390 395 400
Arg Ile Pro Ile His Met Ile Asp Thr Ile Asn Arg Ile Asn Lys Val
405 410 415
Met Arg Lys His Ile Gln Glu Asn Gly Lys Glu Pro Asp Leu Glu Val
420 425 430
Val Ala Glu Glu Val Gly Leu Ser Leu Asp Lys Val Lys Asn Val Ile
435 440 445
Lys Val Thr Lys Glu Pro Ile Ser Leu Glu Thr Pro Val Gly Asn Asp
450 455 460
Asp Asp Gly Lys Phe Gly Asp Phe Val Glu Asp Lys Asn Ile Val Ser
465 470 475 480
Ser Ile Asp His Ile Met Arg Glu Asp Leu Lys Ala Gln Ile Glu Ser
485 490 495
Val Leu Asp Gln Leu Asn Glu Arg Glu Lys Ala Val Ile Arg Met Arg
500 505 510
Phe Gly Leu Leu Asp Asp Glu Ser Asp Arg Thr Leu Glu Glu Ile Gly
515 520 525
Lys Glu Leu Asn Val Thr Arg Glu Arg Val Arg Gln Ile Glu Ser Ser
530 535 540
Ala Ile Lys Lys Leu Arg Ser Pro Gln Tyr Gly Arg Ile Leu Arg Asn
545 550 555 560
Tyr Leu Arg Ile

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<211> 237
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<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(237)
<400> 91

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Lys Leu Val Leu Ala Lys Asn Thr Arg Lys Ser Asp Ala Lys Ser Val
1 5 10 15

gaa tta gag gat ttg tat cac gaa ttc agt gaa gat aag cgt tct att 96
Glu Leu Glu Asp Leu Tyr His Glu Phe Ser Glu Asp Lys Arg Ser Ile
20 25 30

ttc tat ttt gcc ccc aca aac gcc cac aaa gac atg ctc aaa gcg gtg 144
Phe Tyr Phe Ala Pro Thr Asn Ala His Lys Asp Met Leu Lys Ala Val
35 40 45

gat ttt ttc aaa gaa aaa ggt cat acg gct tat tta gat gag gtg agg 192
Asp Phe Phe Lys Glu Lys Gly His Thr Ala Tyr Leu Asp Glu Val Arg

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     50                  55                  60
gtc agc act gat gaa aaa gat ttt ctt tat gaa ttg cac att att       237
Val Ser Thr Asp Glu Lys Asp Phe Leu Tyr Glu Leu His Ile Ile
 65                  70                  75
<210> 92
<211> 79
<212> PRT
<213> Helicobacter pylori
<400> 92
Lys Leu Val Leu Ala Lys Asn Thr Arg Lys Ser Asp Ala Lys Ser Val
  1               5                  10                  15
Glu Leu Glu Asp Leu Tyr His Glu Phe Ser Glu Asp Lys Arg Ser Ile
             20                  25                  30
Phe Tyr Phe Ala Pro Thr Asn Ala His Lys Asp Met Leu Lys Ala Val
         35                  40                  45
Asp Phe Phe Lys Glu Lys Gly His Thr Ala Tyr Leu Asp Glu Val Arg
     50                  55                  60
Val Ser Thr Asp Glu Lys Asp Phe Leu Tyr Glu Leu His Ile Ile
 65                  70                  75
<210> 93
<211> 444
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(444)
<400> 93
gaa ggg gtt tta agg gtt tta ctc aat aaa aag ggc aag ctc att aaa    48
Glu Gly Val Leu Arg Val Leu Leu Asn Lys Lys Gly Lys Leu Ile Lys
  1               5                  10                  15
gaa tac aaa acc tta gag cct tta aaa agc cta gaa atc cgt ttg agt    96
Glu Tyr Lys Thr Leu Glu Pro Leu Lys Ser Leu Glu Ile Arg Leu Ser
             20                  25                  30
gaa gcc ccc att gat aaa cgc aat gat ttt tta tac cat aag acc act   144
Glu Ala Pro Ile Asp Lys Arg Asn Asp Phe Leu Tyr His Lys Thr Thr
         35                  40                  45
tat gcc cct ttt tat caa aag gct cga gcg ctc att aaa aag ggc gtt   192
Tyr Ala Pro Phe Tyr Gln Lys Ala Arg Ala Leu Ile Lys Lys Gly Val
     50                  55                  60
atg ttt gat gaa atc ttt tat aac cag gat ttg gaa ctc act gag ggc   240
Met Phe Asp Glu Ile Phe Tyr Asn Gln Asp Leu Glu Leu Thr Glu Gly
 65                  70                  75                  80
gct agg agc aat ctt gtt tta gaa atc cat aac agg ctt tta acc cct   288
Ala Arg Ser Asn Leu Val Leu Glu Ile His Asn Arg Leu Leu Thr Pro
                 85                  90                  95
tat ttt agc gcg ggc gcg tta aac ggg acg ggt gtt gtg ggg ttg tta   336
Tyr Phe Ser Ala Gly Ala Leu Asn Gly Thr Gly Val Val Gly Leu Leu
            100                 105                 110
aaa aag ggt ctt gtt ggg cat gca cct ttg aaa ttg caa gat ttg caa   384
Lys Lys Gly Leu Val Gly His Ala Pro Leu Lys Leu Gln Asp Leu Gln
        115                 120                 125
aaa gcg tct aaa atc tat tgt att aac gcg cta tat ggc tta gtg gaa   432
Lys Ala Ser Lys Ile Tyr Cys Ile Asn Ala Leu Tyr Gly Leu Val Glu
    130                 135                 140
gtg aaa ata aaa                                                  444
Val Lys Ile Lys
145
<210> 94
<211> 148
<212> PRT
<213> Helicobacter pylori
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<400> 94
Glu Gly Val Leu Arg Val Leu Leu Asn Lys Lys Gly Lys Leu Ile Lys
1 5 10 15
Glu Tyr Lys Thr Leu Glu Pro Leu Lys Ser Leu Glu Ile Arg Leu Ser
20 25 30
Glu Ala Pro Ile Asp Lys Arg Asn Asp Phe Leu Tyr His Lys Thr Thr
35 40 45
Tyr Ala Pro Phe Tyr Gln Lys Ala Arg Ala Leu Ile Lys Lys Gly Val
50 55 60
Met Phe Asp Glu Ile Phe Tyr Asn Gln Asp Leu Glu Leu Thr Glu Gly
65 70 75 80
Ala Arg Ser Asn Leu Val Leu Glu Ile His Asn Arg Leu Leu Thr Pro
85 90 95
Tyr Phe Ser Ala Gly Ala Leu Asn Gly Thr Gly Val Val Gly Leu Leu
100 105 110
Lys Lys Gly Leu Val Gly His Ala Pro Leu Lys Leu Gln Asp Leu Gln
115 120 125
Lys Ala Ser Lys Ile Tyr Cys Ile Asn Ala Leu Tyr Gly Leu Val Glu
130 135 140
Val Lys Ile Lys
145
<210> 95
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<212> DNA
<213> Helicobacter pylori
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<222> (1)..(717)
<400> 95
gca gat gaa acg aac gct ctg aga caa aaa aac aga gaa ctg aac aaa 48
Ala Asp Glu Thr Asn Ala Leu Arg Gln Lys Asn Arg Glu Leu Asn Lys
1 5 10 15
aaa ata gat tgg caa aaa gat tat gac agg gaa aaa tta gaa cga gat 96
Lys Ile Asp Trp Gln Lys Asp Tyr Asp Arg Glu Lys Leu Glu Arg Asp
20 25 30
aat agg gat tta gaa caa tgc aaa gag gat tta tta gcc gct aac gag 144
Asn Arg Asp Leu Glu Gln Cys Lys Glu Asp Leu Leu Ala Ala Asn Glu
35 40 45
aat cta aga aat aga atc caa gaa tgg gaa aat gaa aaa aac aag ctt 192
Asn Leu Arg Asn Arg Ile Gln Glu Trp Glu Asn Glu Lys Asn Lys Leu
50 55 60
gat cca aga gat gaa aga ata aaa gag tta gaa gaa gaa aaa agg gaa 240
Asp Pro Arg Asp Glu Arg Ile Lys Glu Leu Glu Glu Glu Lys Arg Glu
65 70 75 80
tta gag gga att tta gcc caa aaa gag aac gca gaa caa aaa tat aac 288
Leu Glu Gly Ile Leu Ala Gln Lys Glu Asn Ala Glu Gln Lys Tyr Asn
85 90 95
act ctt tca gtc aaa aat aag caa tta gaa gct gag tta gat atg ctt 336
Thr Leu Ser Val Lys Asn Lys Gln Leu Glu Ala Glu Leu Asp Met Leu
100 105 110
aac gaa aaa ttt gaa aaa ctg aaa aat atg tat gct ggg gta gag gat 384
Asn Glu Lys Phe Glu Lys Leu Lys Asn Met Tyr Ala Gly Val Glu Asp
115 120 125
ttt gaa aaa cgc caa aaa aat atc aaa gaa caa att gta aaa acc aac 432
Phe Glu Lys Arg Gln Lys Asn Ile Lys Glu Gln Ile Val Lys Thr Asn
130 135 140
ccc aaa gtc tta ggc gca cct tca aac gaa gtg gaa gaa tta gcg ttc 480
Pro Lys Val Leu Gly Ala Pro Ser Asn Glu Val Glu Glu Leu Ala Phe
145 150 155 160
tta gag cgt ata gaa aag ggc atg caa gag ttc aat gtt ttc tat ccc 528
Leu Glu Arg Ile Glu Lys Gly Met Gln Glu Phe Asn Val Phe Tyr Pro

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                165                 170                 175
aag cgt tta ttg tat atg ttc cac acc gct tta aaa agc acg tct cta   576
Lys Arg Leu Leu Tyr Met Phe His Thr Ala Leu Lys Ser Thr Ser Leu
            180                 185                 190
tcg cca ttg agc gtg cta agt ggg gtg agt ggg aca gga aaa tct gaa   624
Ser Pro Leu Ser Val Leu Ser Gly Val Ser Gly Thr Gly Lys Ser Glu
        195                 200                 205
ctg ccc aag ctc tat gtg cat ttt ggg ggg tta aat ttt tta agc att   672
Leu Pro Lys Leu Tyr Val His Phe Gly Gly Leu Asn Phe Leu Ser Ile
    210                 215                 220
gct gtg cag cct act tgg gat agc cca gaa tcg ttg atg ggg tat tt    719
Ala Val Gln Pro Thr Trp Asp Ser Pro Glu Ser Leu Met Gly Tyr
225                 230                 235
<210> 96
<211> 239
<212> PRT
<213> Helicobacter pylori
<400> 96
Ala Asp Glu Thr Asn Ala Leu Arg Gln Lys Asn Arg Glu Leu Asn Lys
  1               5                  10                  15
Lys Ile Asp Trp Gln Lys Asp Tyr Asp Arg Glu Lys Leu Glu Arg Asp
             20                  25                  30
Asn Arg Asp Leu Glu Gln Cys Lys Glu Asp Leu Leu Ala Ala Asn Glu
         35                  40                  45
Asn Leu Arg Asn Arg Ile Gln Glu Trp Glu Asn Glu Lys Asn Lys Leu
     50                  55                  60
Asp Pro Arg Asp Glu Arg Ile Lys Glu Leu Glu Glu Glu Lys Arg Glu
 65                  70                  75                  80
Leu Glu Gly Ile Leu Ala Gln Lys Glu Asn Ala Glu Gln Lys Tyr Asn
                 85                  90                  95
Thr Leu Ser Val Lys Asn Lys Gln Leu Glu Ala Glu Leu Asp Met Leu
            100                 105                 110
Asn Glu Lys Phe Glu Lys Leu Lys Asn Met Tyr Ala Gly Val Glu Asp
        115                 120                 125
Phe Glu Lys Arg Gln Lys Asn Ile Lys Glu Gln Ile Val Lys Thr Asn
    130                 135                 140
Pro Lys Val Leu Gly Ala Pro Ser Asn Glu Val Glu Glu Leu Ala Phe
145                 150                 155                 160
Leu Glu Arg Ile Glu Lys Gly Met Gln Glu Phe Asn Val Phe Tyr Pro
                165                 170                 175
Lys Arg Leu Leu Tyr Met Phe His Thr Ala Leu Lys Ser Thr Ser Leu
            180                 185                 190
Ser Pro Leu Ser Val Leu Ser Gly Val Ser Gly Thr Gly Lys Ser Glu
        195                 200                 205
Leu Pro Lys Leu Tyr Val His Phe Gly Gly Leu Asn Phe Leu Ser Ile
    210                 215                 220
Ala Val Gln Pro Thr Trp Asp Ser Pro Glu Ser Leu Met Gly Tyr
225                 230                 235
<210> 97
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<212> DNA
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<222> (1)..(819)
<400> 97
aat ggg gtg gag att gta ggg ttg gag cat ttg gat aaa gtg att tat   48
Asn Gly Val Glu Ile Val Gly Leu Glu His Leu Asp Lys Val Ile Tyr
  1               5                  10                  15
tta gat caa gcc ccc ata ggc aaa acc cca cga agc aac cct gcc act   96
Leu Asp Gln Ala Pro Ile Gly Lys Thr Pro Arg Ser Asn Pro Ala Thr
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            20                  25                  30
tac acg gga gtg atg gat gaa atc agg att tta ttt gcc gag caa aaa   144
Tyr Thr Gly Val Met Asp Glu Ile Arg Ile Leu Phe Ala Glu Gln Lys
        35                  40                  45
gaa gct aaa att tta ggc tat agt gcg agc cgt ttt agc ttt aat gtt   192
Glu Ala Lys Ile Leu Gly Tyr Ser Ala Ser Arg Phe Ser Phe Asn Val
    50                  55                  60
aaa gga ggg cgg tgc gag aaa tgc caa ggc gat ggg gac att aaa ata   240
Lys Gly Gly Arg Cys Glu Lys Cys Gln Gly Asp Gly Asp Ile Lys Ile
65                  70                  75                  80
gaa atg cac ttt ttg cct gat gtg tta gtc caa tgc gat agc tgt aag   288
Glu Met His Phe Leu Pro Asp Val Leu Val Gln Cys Asp Ser Cys Lys
                85                  90                  95
ggc gct aaa tac aac ccc caa act tta gaa atc aag gtg aaa ggc aaa   336
Gly Ala Lys Tyr Asn Pro Gln Thr Leu Glu Ile Lys Val Lys Gly Lys
            100                 105                 110
tcc att gcc gat gtg ttg aac atg agc gtg gaa gag gct tat gaa ttt   384
Ser Ile Ala Asp Val Leu Asn Met Ser Val Glu Glu Ala Tyr Glu Phe
        115                 120                 125
ttt gct aaa ttc cct aaa atc gcc gtg aag tta aaa acg ctt atg gat   432
Phe Ala Lys Phe Pro Lys Ile Ala Val Lys Leu Lys Thr Leu Met Asp
    130                 135                 140
gtg ggc tta ggc tat atc act tta ggg caa aac gct acg act tta agt   480
Val Gly Leu Gly Tyr Ile Thr Leu Gly Gln Asn Ala Thr Thr Leu Ser
145                 150                 155                 160
ggg ggg gag gct caa agg atc aaa tta gct aaa gaa ttg agt aaa aaa   528
Gly Gly Glu Ala Gln Arg Ile Lys Leu Ala Lys Glu Leu Ser Lys Lys
                165                 170                 175
gac aca ggc aaa acc ctt tat att tta gat gag cct act acc ggt ttg   576
Asp Thr Gly Lys Thr Leu Tyr Ile Leu Asp Glu Pro Thr Thr Gly Leu
            180                 185                 190
cat ttt gaa gac gtg aat cat ctt tta caa gtc ttg cat tct tta gtg   624
His Phe Glu Asp Val Asn His Leu Leu Gln Val Leu His Ser Leu Val
        195                 200                 205
gcg tta ggc aat tct atg cta gtg att gag cat aat tta gac att atc   672
Ala Leu Gly Asn Ser Met Leu Val Ile Glu His Asn Leu Asp Ile Ile
    210                 215                 220
aaa aac gct gac tac att ata gac atg ggg cct gat ggg ggg gat aag   720
Lys Asn Ala Asp Tyr Ile Ile Asp Met Gly Pro Asp Gly Gly Asp Lys
225                 230                 235                 240
ggc ggg aaa gtc att gcg agc ggc acg cct tta gag gtg gcg caa aat   768
Gly Gly Lys Val Ile Ala Ser Gly Thr Pro Leu Glu Val Ala Gln Asn
                245                 250                 255
tgc gaa aaa acc caa agc tac acg gga aaa ttt tta gct ttg gaa ttg   816
Cys Glu Lys Thr Gln Ser Tyr Thr Gly Lys Phe Leu Ala Leu Glu Leu
            260                 265                 270
aaa                                                               819
Lys
<210> 98
<211> 273
<212> PRT
<213> Helicobacter pylori
<400> 98
Asn Gly Val Glu Ile Val Gly Leu Glu His Leu Asp Lys Val Ile Tyr
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Leu Asp Gln Ala Pro Ile Gly Lys Thr Pro Arg Ser Asn Pro Ala Thr
            20                  25                  30
Tyr Thr Gly Val Met Asp Glu Ile Arg Ile Leu Phe Ala Glu Gln Lys
        35                  40                  45
Glu Ala Lys Ile Leu Gly Tyr Ser Ala Ser Arg Phe Ser Phe Asn Val
    50                  55                  60
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Lys Gly Gly Arg Cys Glu Lys Cys Gln Gly Asp Gly Asp Ile Lys Ile
 65                  70                  75                  80
Glu Met His Phe Leu Pro Asp Val Leu Val Gln Cys Asp Ser Cys Lys
                 85                  90                  95
Gly Ala Lys Tyr Asn Pro Gln Thr Leu Glu Ile Lys Val Lys Gly Lys
            100                 105                 110
Ser Ile Ala Asp Val Leu Asn Met Ser Val Glu Glu Ala Tyr Glu Phe
        115                 120                 125
Phe Ala Lys Phe Pro Lys Ile Ala Val Lys Leu Lys Thr Leu Met Asp
    130                 135                 140
Val Gly Leu Gly Tyr Ile Thr Leu Gly Gln Asn Ala Thr Thr Leu Ser
145                 150                 155                 160
Gly Gly Glu Ala Gln Arg Ile Lys Leu Ala Lys Glu Leu Ser Lys Lys
                165                 170                 175
Asp Thr Gly Lys Thr Leu Tyr Ile Leu Asp Glu Pro Thr Thr Gly Leu
            180                 185                 190
His Phe Glu Asp Val Asn His Leu Leu Gln Val Leu His Ser Leu Val
        195                 200                 205
Ala Leu Gly Asn Ser Met Leu Val Ile Glu His Asn Leu Asp Ile Ile
    210                 215                 220
Lys Asn Ala Asp Tyr Ile Ile Asp Met Gly Pro Asp Gly Gly Asp Lys
225                 230                 235                 240
Gly Gly Lys Val Ile Ala Ser Gly Thr Pro Leu Glu Val Ala Gln Asn
                245                 250                 255
Cys Glu Lys Thr Gln Ser Tyr Thr Gly Lys Phe Leu Ala Leu Glu Leu
            260                 265                 270
Lys
<210> 99
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<212> DNA
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<222> (1)..(1404)
<400> 99
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Gly Phe Leu Arg Ile Leu Asp Val Ile Lys Lys Val Thr Thr Pro Lys
  1               5                  10                  15
ggt ggc att gaa atc tta agg act tta att gat ttt acg ccc aaa att   96
Gly Gly Ile Glu Ile Leu Arg Thr Leu Ile Asp Phe Thr Pro Lys Ile
             20                  25                  30
gaa aac gcc ctg aat tta gcg gcc aaa agc cat aag ggg caa tac aga   144
Glu Asn Ala Leu Asn Leu Ala Ala Lys Ser His Lys Gly Gln Tyr Arg
         35                  40                  45
aaa agc ggc gag cct tat att gtc cat cct att tgc gtg gca agc ttg   192
Lys Ser Gly Glu Pro Tyr Ile Val His Pro Ile Cys Val Ala Ser Leu
     50                  55                  60
gta gcg ttt tgt ggg ggc gat gag gcg atg gtg tgt gct gcg ctt ttg   240
Val Ala Phe Cys Gly Gly Asp Glu Ala Met Val Cys Ala Ala Leu Leu
 65                  70                  75                  80
cat gat gtg gtg gaa gac acg cct tgt aag att gaa acg att gag caa   288
His Asp Val Val Glu Asp Thr Pro Cys Lys Ile Glu Thr Ile Glu Gln
                 85                  90                  95
gaa ttt ggg caa gat gtg gct aat tta gtg gat gcg ctc act aaa atc   336
Glu Phe Gly Gln Asp Val Ala Asn Leu Val Asp Ala Leu Thr Lys Ile
            100                 105                 110
act gaa atc agg aaa gaa gaa tta ggc gtg agc tct caa gat ccc aga   384
Thr Glu Ile Arg Lys Glu Glu Leu Gly Val Ser Ser Gln Asp Pro Arg
        115                 120                 125
atg gtg gtt tca gcg ctc act ttc aga aag att tta att agc gcg ata   432
Met Val Val Ser Ala Leu Thr Phe Arg Lys Ile Leu Ile Ser Ala Ile
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    130                 135                 140
caa gat cca aga gcc tta gtg gta aag att agc gac agg ttg cac aac  480
Gln Asp Pro Arg Ala Leu Val Val Lys Ile Ser Asp Arg Leu His Asn
145                 150                 155                 160
atg ctc acc tta gac gcc ttg cct cat gac aag caa gtg cgt att tct  528
Met Leu Thr Leu Asp Ala Leu Pro His Asp Lys Gln Val Arg Ile Ser
                165                 170                 175
aaa gag act cta gcg gtg tat gcc cct ata gcg agc cga ttg ggc atg  576
Lys Glu Thr Leu Ala Val Tyr Ala Pro Ile Ala Ser Arg Leu Gly Met
            180                 185                 190
tct tca atc aaa aat gaa tta gaa gac aag agc ttt tat tat att tat  624
Ser Ser Ile Lys Asn Glu Leu Glu Asp Lys Ser Phe Tyr Tyr Ile Tyr
        195                 200                 205
cca gaa gag tat aaa aat atc aag gaa tat ttg cac aaa aac aag cag  672
Pro Glu Glu Tyr Lys Asn Ile Lys Glu Tyr Leu His Lys Asn Lys Gln
    210                 215                 220
tct tta ctc tta aag ctc aac gct ttt gcg agc aag tta gaa aaa aaa  720
Ser Leu Leu Leu Lys Leu Asn Ala Phe Ala Ser Lys Leu Glu Lys Lys
225                 230                 235                 240
ctt ttt gat agt ggg ttt agc cat tcg gat ttt aaa ctc gtt aca agg  768
Leu Phe Asp Ser Gly Phe Ser His Ser Asp Phe Lys Leu Val Thr Arg
                245                 250                 255
gtg aaa cgc cct tat tct atc tat ctt aag atg caa cga aag ggc gcg  816
Val Lys Arg Pro Tyr Ser Ile Tyr Leu Lys Met Gln Arg Lys Gly Ala
            260                 265                 270
gtt aat att gat gaa att ttg gac ttg tta gcc att agg att tta ttg  864
Val Asn Ile Asp Glu Ile Leu Asp Leu Leu Ala Ile Arg Ile Leu Leu
        275                 280                 285
aaa aac ccg att gat tgc tat aaa gtt tta ggg att atc cat ttg aat  912
Lys Asn Pro Ile Asp Cys Tyr Lys Val Leu Gly Ile Ile His Leu Asn
    290                 295                 300
ttc aaa ccc att gtc tct cgt ttt aaa gat tac atc gct ttg ccc aaa  960
Phe Lys Pro Ile Val Ser Arg Phe Lys Asp Tyr Ile Ala Leu Pro Lys
305                 310                 315                 320
gaa aat ggc tat aag acg ata cac acg acc att ttt gat gaa tct tct 1008
Glu Asn Gly Tyr Lys Thr Ile His Thr Thr Ile Phe Asp Glu Ser Ser
                325                 330                 335
gtt tat gaa gtg cag atc cgc acc ttt gat atg cat atg ggg gcg gag 1056
Val Tyr Glu Val Gln Ile Arg Thr Phe Asp Met His Met Gly Ala Glu
            340                 345                 350
tat ggt aat tca gcc cac tgg aag tat aaa gcc ggg ggc gtg gat cat 1104
Tyr Gly Asn Ser Ala His Trp Lys Tyr Lys Ala Gly Gly Val Asp His
        355                 360                 365
gaa gat cat cat gag ggc atg aga tgg ttg caa aat ttt aaa tac cat 1152
Glu Asp His His Glu Gly Met Arg Trp Leu Gln Asn Phe Lys Tyr His
    370                 375                 380
gac agc gat ttg aaa aac gac cct aag gaa ttt tac gaa ctc gct aag 1200
Asp Ser Asp Leu Lys Asn Asp Pro Lys Glu Phe Tyr Glu Leu Ala Lys
385                 390                 395                 400
aac gat ttg tat cgt gaa gat att gtc gtt ttt tcg cct cat ggg gac 1248
Asn Asp Leu Tyr Arg Glu Asp Ile Val Val Phe Ser Pro His Gly Asp
                405                 410                 415
act tac act tta ccg gtg ggt gcg atc gct tta gat ttt gct tac atg 1296
Thr Tyr Thr Leu Pro Val Gly Ala Ile Ala Leu Asp Phe Ala Tyr Met
            420                 425                 430
gtg cat agc gat ttg ggc gat aaa gcc acg gac gct tat atc aat agt 1344
Val His Ser Asp Leu Gly Asp Lys Ala Thr Asp Ala Tyr Ile Asn Ser
        435                 440                 445
aaa aaa gcc tta ctc aat cag gaa tta aga agt ggg gat gtg gtt aaa 1392
Lys Lys Ala Leu Leu Asn Gln Glu Leu Arg Ser Gly Asp Val Val Lys
    450                 455                 460
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1405

atc att aaa ggc g
Ile Ile Lys Gly
465
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<212> PRT
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Gly Phe Leu Arg Ile Leu Asp Val Ile Lys Lys Val Thr Thr Pro Lys
  1               5                  10                  15
Gly Gly Ile Glu Ile Leu Arg Thr Leu Ile Asp Phe Thr Pro Lys Ile
             20                  25                  30
Glu Asn Ala Leu Asn Leu Ala Ala Lys Ser His Lys Gly Gln Tyr Arg
         35                  40                  45
Lys Ser Gly Glu Pro Tyr Ile Val His Pro Ile Cys Val Ala Ser Leu
     50                  55                  60
Val Ala Phe Cys Gly Gly Asp Glu Ala Met Val Cys Ala Ala Leu Leu
 65                  70                  75                  80
His Asp Val Val Glu Asp Thr Pro Cys Lys Ile Glu Thr Ile Glu Gln
                 85                  90                  95
Glu Phe Gly Gln Asp Val Ala Asn Leu Val Asp Ala Leu Thr Lys Ile
            100                 105                 110
Thr Glu Ile Arg Lys Glu Glu Leu Gly Val Ser Ser Gln Asp Pro Arg
        115                 120                 125
Met Val Val Ser Ala Leu Thr Phe Arg Lys Ile Leu Ile Ser Ala Ile
    130                 135                 140
Gln Asp Pro Arg Ala Leu Val Val Lys Ile Ser Asp Arg Leu His Asn
145                 150                 155                 160
Met Leu Thr Leu Asp Ala Leu Pro His Asp Lys Gln Val Arg Ile Ser
                165                 170                 175
Lys Glu Thr Leu Ala Val Tyr Ala Pro Ile Ala Ser Arg Leu Gly Met
            180                 185                 190
Ser Ser Ile Lys Asn Glu Leu Glu Asp Lys Ser Phe Tyr Tyr Ile Tyr
        195                 200                 205
Pro Glu Glu Tyr Lys Asn Ile Lys Glu Tyr Leu His Lys Asn Lys Gln
    210                 215                 220
Ser Leu Leu Leu Lys Leu Asn Ala Phe Ala Ser Lys Leu Glu Lys Lys
225                 230                 235                 240
Leu Phe Asp Ser Gly Phe Ser His Ser Asp Phe Lys Leu Val Thr Arg
                245                 250                 255
Val Lys Arg Pro Tyr Ser Ile Tyr Leu Lys Met Gln Arg Lys Gly Ala
            260                 265                 270
Val Asn Ile Asp Glu Ile Leu Asp Leu Leu Ala Ile Arg Ile Leu Leu
        275                 280                 285
Lys Asn Pro Ile Asp Cys Tyr Lys Val Leu Gly Ile Ile His Leu Asn
    290                 295                 300
Phe Lys Pro Ile Val Ser Arg Phe Lys Asp Tyr Ile Ala Leu Pro Lys
305                 310                 315                 320
Glu Asn Gly Tyr Lys Thr Ile His Thr Thr Ile Phe Asp Glu Ser Ser
                325                 330                 335
Val Tyr Glu Val Gln Ile Arg Thr Phe Asp Met His Met Gly Ala Glu
            340                 345                 350
Tyr Gly Asn Ser Ala His Trp Lys Tyr Lys Ala Gly Gly Val Asp His
        355                 360                 365
Glu Asp His His Glu Gly Met Arg Trp Leu Gln Asn Phe Lys Tyr His
    370                 375                 380
Asp Ser Asp Leu Lys Asn Asp Pro Lys Glu Phe Tyr Glu Leu Ala Lys
385                 390                 395                 400
Asn Asp Leu Tyr Arg Glu Asp Ile Val Val Phe Ser Pro His Gly Asp
                405                 410                 415
Thr Tyr Thr Leu Pro Val Gly Ala Ile Ala Leu Asp Phe Ala Tyr Met
```

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          420                 425                 430
Val His Ser Asp Leu Gly Asp Lys Ala Thr Asp Ala Tyr Ile Asn Ser
        435                 440                 445
Lys Lys Ala Leu Leu Asn Gln Glu Leu Arg Ser Gly Asp Val Val Lys
    450                 455                 460
Ile Ile Lys Gly
465
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<211> 822
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<213> Helicobacter pylori
<220>
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Pro Lys Glu Arg Val Leu Ser Asp Glu Glu Ile Asn Asn Arg Ala Glu
  1               5                  10                  15
agg atc gct aaa agc gag tta gag aag gat acg aag ctc gtt tca tca   96
Arg Ile Ala Lys Ser Glu Leu Glu Lys Asp Thr Lys Leu Val Ser Ser
             20                  25                  30
cac gat caa tac gag cgc atg aaa aaa agc gga tcg ctc aac acg gaa   144
His Asp Gln Tyr Glu Arg Met Lys Lys Ser Gly Ser Leu Asn Thr Glu
         35                  40                  45
aac tta gat tcg cac att caa gcc aac agc tta caa gag ctg aat caa   192
Asn Leu Asp Ser His Ile Gln Ala Asn Ser Leu Gln Glu Leu Asn Gln
     50                  55                  60
aaa ttg ctc caa ttc gtg ggc gcg gat agg aag tat atg ccc tac act   240
Lys Leu Leu Gln Phe Val Gly Ala Asp Arg Lys Tyr Met Pro Tyr Thr
 65                  70                  75                  80
aaa gcg gtg caa att tct ttg aat aac ccc aat ctt aaa gat ttg gaa   288
Lys Ala Val Gln Ile Ser Leu Asn Asn Pro Asn Leu Lys Asp Leu Glu
                 85                  90                  95
gtg att gac acc cca gga gtg aat gac ccc atc gct tcc agg gaa gaa   336
Val Ile Asp Thr Pro Gly Val Asn Asp Pro Ile Ala Ser Arg Glu Glu
            100                 105                 110
cgc acc aaa gcc tta ttg aaa gat tgc gat gtg gtg ttt atc ata agc   384
Arg Thr Lys Ala Leu Leu Lys Asp Cys Asp Val Val Phe Ile Ile Ser
        115                 120                 125
tct tct aat cag ttt tta acg gag agc gat atg agt ttg ttt gac agg   432
Ser Ser Asn Gln Phe Leu Thr Glu Ser Asp Met Ser Leu Phe Asp Arg
    130                 135                 140
gtt tct aac aaa gaa agc ctt caa gaa att tat ttt gtg gca agc caa   480
Val Ser Asn Lys Glu Ser Leu Gln Glu Ile Tyr Phe Val Ala Ser Gln
145                 150                 155                 160
gcc gat agc gct gtt ctt tct atg agt gaa gtg gaa aaa tct cgc cac   528
Ala Asp Ser Ala Val Leu Ser Met Ser Glu Val Glu Lys Ser Arg His
                165                 170                 175
cac ctc ccc aca gcc tta gaa aac gcg caa aaa tcc ctt tca tct tct   576
His Leu Pro Thr Ala Leu Glu Asn Ala Gln Lys Ser Leu Ser Ser Ser
            180                 185                 190
tta aat aaa acc atg gaa gca ttg att caa aca aac cct aac caa cga   624
Leu Asn Lys Thr Met Glu Ala Leu Ile Gln Thr Asn Pro Asn Gln Arg
        195                 200                 205
ggg att ttt gaa aaa gcg atc aaa aac ggc gtc att ttg act tca ggg   672
Gly Ile Phe Glu Lys Ala Ile Lys Asn Gly Val Ile Leu Thr Ser Gly
    210                 215                 220
gct tgc ttt agc atg tat aag gat ttc aaa aac caa gct tct tgg gaa   720
Ala Cys Phe Ser Met Tyr Lys Asp Phe Lys Asn Gln Ala Ser Trp Glu
225                 230                 235                 240
agc aaa aaa gaa gag tgt tac aat gca tgg cgg aat tta acc aac gct   768
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Ser Lys Lys Glu Glu Cys Tyr Asn Ala Trp Arg Asn Leu Thr Asn Ala
                245                 250                 255
tac ccc ctg acg ctt tta aca gcg ttg ata aat ctg aag aaa gct tat   816
Tyr Pro Leu Thr Leu Leu Thr Ala Leu Ile Asn Leu Lys Lys Ala Tyr
            260                 265                 270
tat tct                                                           822
Tyr Ser
<210> 102
<211> 274
<212> PRT
<213> Helicobacter pylori
<400> 102
Pro Lys Glu Arg Val Leu Ser Asp Glu Glu Ile Asn Asn Arg Ala Glu
  1               5                  10                  15
Arg Ile Ala Lys Ser Glu Leu Glu Lys Asp Thr Lys Leu Val Ser Ser
             20                  25                  30
His Asp Gln Tyr Glu Arg Met Lys Lys Ser Gly Ser Leu Asn Thr Glu
         35                  40                  45
Asn Leu Asp Ser His Ile Gln Ala Asn Ser Leu Gln Glu Leu Asn Gln
     50                  55                  60
Lys Leu Leu Gln Phe Val Gly Ala Asp Arg Lys Tyr Met Pro Tyr Thr
 65                  70                  75                  80
Lys Ala Val Gln Ile Ser Leu Asn Asn Pro Asn Leu Lys Asp Leu Glu
                 85                  90                  95
Val Ile Asp Thr Pro Gly Val Asn Asp Pro Ile Ala Ser Arg Glu Glu
            100                 105                 110
Arg Thr Lys Ala Leu Leu Lys Asp Cys Asp Val Val Phe Ile Ile Ser
        115                 120                 125
Ser Ser Asn Gln Phe Leu Thr Glu Ser Asp Met Ser Leu Phe Asp Arg
    130                 135                 140
Val Ser Asn Lys Glu Ser Leu Gln Glu Ile Tyr Phe Val Ala Ser Gln
145                 150                 155                 160
Ala Asp Ser Ala Val Leu Ser Met Ser Glu Val Glu Lys Ser Arg His
                165                 170                 175
His Leu Pro Thr Ala Leu Glu Asn Ala Gln Lys Ser Leu Ser Ser Ser
            180                 185                 190
Leu Asn Lys Thr Met Glu Ala Leu Ile Gln Thr Asn Pro Asn Gln Arg
        195                 200                 205
Gly Ile Phe Glu Lys Ala Ile Lys Asn Gly Val Ile Leu Thr Ser Gly
    210                 215                 220
Ala Cys Phe Ser Met Tyr Lys Asp Phe Lys Asn Gln Ala Ser Trp Glu
225                 230                 235                 240
Ser Lys Lys Glu Glu Cys Tyr Asn Ala Trp Arg Asn Leu Thr Asn Ala
                245                 250                 255
Tyr Pro Leu Thr Leu Leu Thr Ala Leu Ile Asn Leu Lys Lys Ala Tyr
            260                 265                 270
Tyr Ser
<210> 103
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<212> DNA
<213> Helicobacter pylori
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<221> CDS
<222> (1)..(711)
<400> 103
agc gaa aaa aat ata gaa aag gtt ttg aac gcc tat gat aag caa caa    48
Ser Glu Lys Asn Ile Glu Lys Val Leu Asn Ala Tyr Asp Lys Gln Gln
  1               5                  10                  15
cac cac cat caa gac gat ctc gct att cag tat tta cca gcc gtg cgc    96
His His His Gln Asp Asp Leu Ala Ile Gln Tyr Leu Pro Ala Val Arg
             20                  25                  30
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gcc atg gcg ttt cgt cta aaa gag cgc ttg ccc agc tct att gat ttt   144
Ala Met Ala Phe Arg Leu Lys Glu Arg Leu Pro Ser Ser Ile Asp Phe
         35                  40                  45
aac gat ctg gtt tct att ggc act gaa gaa ttg att aaa tta gcc agg   192
Asn Asp Leu Val Ser Ile Gly Thr Glu Glu Leu Ile Lys Leu Ala Arg
     50                  55                  60
cgt tat gag agc gcg tta aac gat tct ttt tgg ggg tat gcg aag act   240
Arg Tyr Glu Ser Ala Leu Asn Asp Ser Phe Trp Gly Tyr Ala Lys Thr
 65                  70                  75                  80
cgt gtc aat ggg gcg atg tta gat tat ttg cgc tct tta gat gtg att   288
Arg Val Asn Gly Ala Met Leu Asp Tyr Leu Arg Ser Leu Asp Val Ile
                 85                  90                  95
tct cgc tct agc agg aaa ctc att aaa agc att gat att gaa atc acc   336
Ser Arg Ser Ser Arg Lys Leu Ile Lys Ser Ile Asp Ile Glu Ile Thr
            100                 105                 110
aaa cac ctt aat gag cat ggg aaa gag cct agc gat gcg tat tta gcg   384
Lys His Leu Asn Glu His Gly Lys Glu Pro Ser Asp Ala Tyr Leu Ala
        115                 120                 125
caa act tta ggc gaa aat att gaa aaa att aaa gaa gcc aaa acg gct   432
Gln Thr Leu Gly Glu Asn Ile Glu Lys Ile Lys Glu Ala Lys Thr Ala
    130                 135                 140
tca gat att tat gcg tta gtg cca ata gat gaa caa ttc aat gcg att   480
Ser Asp Ile Tyr Ala Leu Val Pro Ile Asp Glu Gln Phe Asn Ala Ile
145                 150                 155                 160
gag caa gat gaa atc act aaa aaa att gaa gca gaa gag ttg tta gag   528
Glu Gln Asp Glu Ile Thr Lys Lys Ile Glu Ala Glu Glu Leu Leu Glu
                165                 170                 175
cat gtc caa aaa gcg ctg aat caa atg agc gaa aga gag caa atc ctt   576
His Val Gln Lys Ala Leu Asn Gln Met Ser Glu Arg Glu Gln Ile Leu
            180                 185                 190
atc cag ctt tat tac ttt gaa gag ttg aat ttg agc gag att aaa gag   624
Ile Gln Leu Tyr Tyr Phe Glu Glu Leu Asn Leu Ser Glu Ile Lys Glu
        195                 200                 205
att tta ggc att act gaa tcg cgc att tct caa atc att aaa gaa gtg   672
Ile Leu Gly Ile Thr Glu Ser Arg Ile Ser Gln Ile Ile Lys Glu Val
    210                 215                 220
att aaa aag gtg cgt aaa tcc tta gga gtg gat cat ggc               711
Ile Lys Lys Val Arg Lys Ser Leu Gly Val Asp His Gly
225                 230                 235
<210> 104
<211> 237
<212> PRT
<213> Helicobacter pylori
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Ser Glu Lys Asn Ile Glu Lys Val Leu Asn Ala Tyr Asp Lys Gln Gln
  1               5                  10                  15
His His His Gln Asp Asp Leu Ala Ile Gln Tyr Leu Pro Ala Val Arg
             20                  25                  30
Ala Met Ala Phe Arg Leu Lys Glu Arg Leu Pro Ser Ser Ile Asp Phe
         35                  40                  45
Asn Asp Leu Val Ser Ile Gly Thr Glu Glu Leu Ile Lys Leu Ala Arg
     50                  55                  60
Arg Tyr Glu Ser Ala Leu Asn Asp Ser Phe Trp Gly Tyr Ala Lys Thr
 65                  70                  75                  80
Arg Val Asn Gly Ala Met Leu Asp Tyr Leu Arg Ser Leu Asp Val Ile
                 85                  90                  95
Ser Arg Ser Ser Arg Lys Leu Ile Lys Ser Ile Asp Ile Glu Ile Thr
            100                 105                 110
Lys His Leu Asn Glu His Gly Lys Glu Pro Ser Asp Ala Tyr Leu Ala
        115                 120                 125
Gln Thr Leu Gly Glu Asn Ile Glu Lys Ile Lys Glu Ala Lys Thr Ala
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    130                 135                 140
Ser Asp Ile Tyr Ala Leu Val Pro Ile Asp Glu Gln Phe Asn Ala Ile
145                 150                 155                 160
Glu Gln Asp Glu Ile Thr Lys Lys Ile Glu Ala Glu Glu Leu Leu Glu
                165                 170                 175
His Val Gln Lys Ala Leu Asn Gln Met Ser Glu Arg Glu Gln Ile Leu
            180                 185                 190
Ile Gln Leu Tyr Tyr Phe Glu Glu Leu Asn Leu Ser Glu Ile Lys Glu
        195                 200                 205
Ile Leu Gly Ile Thr Glu Ser Arg Ile Ser Gln Ile Ile Lys Glu Val
    210                 215                 220
Ile Lys Lys Val Arg Lys Ser Leu Gly Val Asp His Gly
225                 230                 235
<210> 105
<211> 1134
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<220>
<221> CDS
<222> (1)..(1134)
<400> 105
gaa tac aac cgc ctc aaa caa cgc acc gag cat gat tta gaa atg att   48
Glu Tyr Asn Arg Leu Lys Gln Arg Thr Glu His Asp Leu Glu Met Ile
  1               5                  10                  15
agc gcg acc ggt gtg tgt aag ggc att gaa aat tac gcg cgc cat ttc   96
Ser Ala Thr Gly Val Cys Lys Gly Ile Glu Asn Tyr Ala Arg His Phe
             20                  25                  30
acc ggt aaa gcc cct aac gaa acg cct ttt tgc ttg ttt gat tat tta   144
Thr Gly Lys Ala Pro Asn Glu Thr Pro Phe Cys Leu Phe Asp Tyr Leu
         35                  40                  45
ggg att ttt gag cgg gag ttt tta gtc att gtg gat gaa agc cat gtg   192
Gly Ile Phe Glu Arg Glu Phe Leu Val Ile Val Asp Glu Ser His Val
     50                  55                  60
agt ttg cca cag ttt ggg ggg atg tat gca ggg gat atg agc agg aaa   240
Ser Leu Pro Gln Phe Gly Gly Met Tyr Ala Gly Asp Met Ser Arg Lys
 65                  70                  75                  80
agt gtt tta gtg gaa tat ggt ttt aga ttg cct agc gct tta gac aac   288
Ser Val Leu Val Glu Tyr Gly Phe Arg Leu Pro Ser Ala Leu Asp Asn
                 85                  90                  95
cgc cct tta aaa ttt gat gaa ttt atc cat aaa aat tgc cag ttc ctt   336
Arg Pro Leu Lys Phe Asp Glu Phe Ile His Lys Asn Cys Gln Phe Leu
            100                 105                 110
ttt gtg tcc gct acg ccc aat aag cta gaa tta gag ctt tcc aaa aag   384
Phe Val Ser Ala Thr Pro Asn Lys Leu Glu Leu Glu Leu Ser Lys Lys
        115                 120                 125
aat gtc gct gag caa atc att cgc cct aca ggg ctt tta gac cct aaa   432
Asn Val Ala Glu Gln Ile Ile Arg Pro Thr Gly Leu Leu Asp Pro Lys
    130                 135                 140
ttt gaa gtg cga gac agc gat aag caa gtc cag gat ttg ttt gat gaa   480
Phe Glu Val Arg Asp Ser Asp Lys Gln Val Gln Asp Leu Phe Asp Glu
145                 150                 155                 160
atc aag tta gtg gtg gct aga ggt gaa agg gtg ctc atc acc acg ctc   528
Ile Lys Leu Val Val Ala Arg Gly Glu Arg Val Leu Ile Thr Thr Leu
                165                 170                 175
act aaa aaa atg gca gaa gaa ttg tgc aaa tat tat gct gaa tgg ggc   576
Thr Lys Lys Met Ala Glu Glu Leu Cys Lys Tyr Tyr Ala Glu Trp Gly
            180                 185                 190
ttg aag gcg cgt tac atg cat agt gaa att gat gcg att gaa agg aat   624
Leu Lys Ala Arg Tyr Met His Ser Glu Ile Asp Ala Ile Glu Arg Asn
        195                 200                 205
cac atc atc cgc tct tta agg ctt aaa gaa ttt gac att tta ata ggg   672
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His Ile Ile Arg Ser Leu Arg Leu Lys Glu Phe Asp Ile Leu Ile Gly
    210                 215                 220
atc aat ctt tta aga gaa ggg ctg gat ttg cct gaa gtc tct tta gta   720
Ile Asn Leu Leu Arg Glu Gly Leu Asp Leu Pro Glu Val Ser Leu Val
225                 230                 235                 240
gcg atc atg gat gcg gat aaa gaa ggg ttt tta agg agt gaa aca agc   768
Ala Ile Met Asp Ala Asp Lys Glu Gly Phe Leu Arg Ser Glu Thr Ser
                245                 250                 255
ctc att caa acc atg ggg cga gcc gct aga aac gct aat ggc aag gtt   816
Leu Ile Gln Thr Met Gly Arg Ala Ala Arg Asn Ala Asn Gly Lys Val
            260                 265                 270
tta tta tac gct aaa aag atc act caa agc atg caa aaa gcc ttt gag   864
Leu Leu Tyr Ala Lys Lys Ile Thr Gln Ser Met Gln Lys Ala Phe Glu
        275                 280                 285
atc act agt tac agg cgc gcc aaa caa gaa gag ttc aat aaa atc cat   912
Ile Thr Ser Tyr Arg Arg Ala Lys Gln Glu Glu Phe Asn Lys Ile His
    290                 295                 300
aac atc acc ccc aaa acc gtt acg cgc gct tta gaa gag gaa ttg aaa   960
Asn Ile Thr Pro Lys Thr Val Thr Arg Ala Leu Glu Glu Glu Leu Lys
305                 310                 315                 320
tta aga gac gat gaa att aga atc gct aaa gcc tta aaa aag gac aaa   1008
Leu Arg Asp Asp Glu Ile Arg Ile Ala Lys Ala Leu Lys Lys Asp Lys
                325                 330                 335
atg cct aaa agt gaa agg gaa aaa atc att aaa gaa ttg gat aaa aaa   1056
Met Pro Lys Ser Glu Arg Glu Lys Ile Ile Lys Glu Leu Asp Lys Lys
            340                 345                 350
atg cga gaa tgc acg aag aat ttg gat ttt gaa gaa gcg atg cgt ttg   1104
Met Arg Glu Cys Thr Lys Asn Leu Asp Phe Glu Glu Ala Met Arg Leu
        355                 360                 365
aga gac gaa atc gct caa tta aga acg ctt                          1134
Arg Asp Glu Ile Ala Gln Leu Arg Thr Leu
    370                 375
<210> 106
<211> 378
<212> PRT
<213> Helicobacter pylori
<400> 106
Glu Tyr Asn Arg Leu Lys Gln Arg Thr Glu His Asp Leu Glu Met Ile
  1               5                  10                  15
Ser Ala Thr Gly Val Cys Lys Gly Ile Glu Asn Tyr Ala Arg His Phe
            20                  25                  30
Thr Gly Lys Ala Pro Asn Glu Thr Pro Phe Cys Leu Phe Asp Tyr Leu
        35                  40                  45
Gly Ile Phe Glu Arg Glu Phe Leu Val Ile Val Asp Glu Ser His Val
    50                  55                  60
Ser Leu Pro Gln Phe Gly Gly Met Tyr Ala Gly Asp Met Ser Arg Lys
65                  70                  75                  80
Ser Val Leu Val Glu Tyr Gly Phe Arg Leu Pro Ser Ala Leu Asp Asn
                85                  90                  95
Arg Pro Leu Lys Phe Asp Glu Phe Ile His Lys Asn Cys Gln Phe Leu
            100                 105                 110
Phe Val Ser Ala Thr Pro Asn Lys Leu Glu Leu Glu Leu Ser Lys Lys
        115                 120                 125
Asn Val Ala Glu Gln Ile Ile Arg Pro Thr Gly Leu Leu Asp Pro Lys
    130                 135                 140
Phe Glu Val Arg Asp Ser Asp Lys Gln Val Gln Asp Leu Phe Asp Glu
145                 150                 155                 160
Ile Lys Leu Val Val Ala Arg Gly Glu Arg Val Leu Ile Thr Thr Leu
                165                 170                 175
Thr Lys Lys Met Ala Glu Glu Leu Cys Lys Tyr Tyr Ala Glu Trp Gly
            180                 185                 190
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Leu Lys Ala Arg Tyr Met His Ser Glu Ile Asp Ala Ile Glu Arg Asn
        195                 200                 205
His Ile Ile Arg Ser Leu Arg Leu Lys Glu Phe Asp Ile Leu Ile Gly
    210                 215                 220
Ile Asn Leu Leu Arg Glu Gly Leu Asp Leu Pro Glu Val Ser Leu Val
225                 230                 235                 240
Ala Ile Met Asp Ala Asp Lys Glu Gly Phe Leu Arg Ser Glu Thr Ser
                245                 250                 255
Leu Ile Gln Thr Met Gly Arg Ala Ala Arg Asn Ala Asn Gly Lys Val
            260                 265                 270
Leu Leu Tyr Ala Lys Lys Ile Thr Gln Ser Met Gln Lys Ala Phe Glu
        275                 280                 285
Ile Thr Ser Tyr Arg Arg Ala Lys Gln Glu Glu Phe Asn Lys Ile His
    290                 295                 300
Asn Ile Thr Pro Lys Thr Val Thr Arg Ala Leu Glu Glu Glu Leu Lys
305                 310                 315                 320
Leu Arg Asp Asp Glu Ile Arg Ile Ala Lys Ala Leu Lys Lys Asp Lys
                325                 330                 335
Met Pro Lys Ser Glu Arg Glu Lys Ile Ile Lys Glu Leu Asp Lys Lys
            340                 345                 350
Met Arg Glu Cys Thr Lys Asn Leu Asp Phe Glu Glu Ala Met Arg Leu
        355                 360                 365
Arg Asp Glu Ile Ala Gln Leu Arg Thr Leu
    370                 375
<210> 107
<211> 499
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<213> Helicobacter pylori
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<400> 107
gaa tcc tta cga gcc tta aaa gct tcg caa gaa gtg cag gct aac acg   48
Glu Ser Leu Arg Ala Leu Lys Ala Ser Gln Glu Val Gln Ala Asn Thr
  1               5                  10                  15
ctt aag cag caa tcg caa act tta gag gat ttg agg aat gag att cac   96
Leu Lys Gln Gln Ser Gln Thr Leu Glu Asp Leu Arg Asn Glu Ile His
            20                  25                  30
gct aac cag caa gct atc cag cag tta gac aag caa aat aaa gag atg   144
Ala Asn Gln Gln Ala Ile Gln Gln Leu Asp Lys Gln Asn Lys Glu Met
        35                  40                  45
agt gaa tta ttg acc aag tta agc cag gat ttg gtt tca caa atc gcc   192
Ser Glu Leu Leu Thr Lys Leu Ser Gln Asp Leu Val Ser Gln Ile Ala
    50                  55                  60
tta atc caa aaa gct ctc aaa gaa caa gag gaa aaa gct gaa aag ccg   240
Leu Ile Gln Lys Ala Leu Lys Glu Gln Glu Glu Lys Ala Glu Lys Pro
65                  70                  75                  80
ctc aaa tca aac gct ccg gct aat aaa acc ccc tct ttg aaa gcc gaa   288
Leu Lys Ser Asn Ala Pro Ala Asn Lys Thr Pro Ser Leu Lys Ala Glu
                85                  90                  95
tcc cca aaa aat caa gag gga aaa act caa gaa aag gcg aaa att gag   336
Ser Pro Lys Asn Gln Glu Gly Lys Thr Gln Glu Lys Ala Lys Ile Glu
            100                 105                 110
ttt gat aaa gac ttg tct aag caa aaa gag atc ttt caa gaa gct ctg   384
Phe Asp Lys Asp Leu Ser Lys Gln Lys Glu Ile Phe Gln Glu Ala Leu
        115                 120                 125
tct ttt ttt aaa aat aaa tcc tat gca gaa gcc aaa gag cgt ttg ttg   432
Ser Phe Phe Lys Asn Lys Ser Tyr Ala Glu Ala Lys Glu Arg Leu Leu
    130                 135                 140
tgg tta gaa gcc aat agt tac aga ctt tat tat gtg cgt tat gtt ctt   480
Trp Leu Glu Ala Asn Ser Tyr Arg Leu Tyr Tyr Val Arg Tyr Val Leu
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145 150 155 160
gga gaa gtg gct tat ggg g 499
Gly Glu Val Ala Tyr Gly
165

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<211> 166
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<213> Helicobacter pylori
<400> 108
Glu Ser Leu Arg Ala Leu Lys Ala Ser Gln Glu Val Gln Ala Asn Thr
1 5 10 15
Leu Lys Gln Gln Ser Gln Thr Leu Glu Asp Leu Arg Asn Glu Ile His
20 25 30
Ala Asn Gln Gln Ala Ile Gln Gln Leu Asp Lys Gln Asn Lys Glu Met
35 40 45
Ser Glu Leu Leu Thr Lys Leu Ser Gln Asp Leu Val Ser Gln Ile Ala
50 55 60
Leu Ile Gln Lys Ala Leu Lys Glu Gln Glu Glu Lys Ala Glu Lys Pro
65 70 75 80
Leu Lys Ser Asn Ala Pro Ala Asn Lys Thr Pro Ser Leu Lys Ala Glu
85 90 95
Ser Pro Lys Asn Gln Glu Gly Lys Thr Gln Glu Lys Ala Lys Ile Glu
100 105 110
Phe Asp Lys Asp Leu Ser Lys Gln Lys Glu Ile Phe Gln Glu Ala Leu
115 120 125
Ser Phe Phe Lys Asn Lys Ser Tyr Ala Glu Ala Lys Glu Arg Leu Leu
130 135 140
Trp Leu Glu Ala Asn Ser Tyr Arg Leu Tyr Tyr Val Arg Tyr Val Leu
145 150 155 160
Gly Glu Val Ala Tyr Gly
165

<210> 109
<211> 133
<212> DNA
<213> Helicobacter pylori
<220>
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<222> (1)..(132)
<400> 109
cac act cta aaa gaa atg ctc acc att aaa tcc gat gat att aga ggc 48
His Thr Leu Lys Glu Met Leu Thr Ile Lys Ser Asp Asp Ile Arg Gly
1 5 10 15
aga gag aac gct tat agg gct atc gct aaa ggt gag caa gtg ggc gag 96
Arg Glu Asn Ala Tyr Arg Ala Ile Ala Lys Gly Glu Gln Val Gly Glu
20 25 30
agt gaa atc cct gag act ttc tat gtt ttg act aaa g 133
Ser Glu Ile Pro Glu Thr Phe Tyr Val Leu Thr Lys
35 40

<210> 110
<211> 44
<212> PRT
<213> Helicobacter pylori
<400> 110
His Thr Leu Lys Glu Met Leu Thr Ile Lys Ser Asp Asp Ile Arg Gly
1 5 10 15
Arg Glu Asn Ala Tyr Arg Ala Ile Ala Lys Gly Glu Gln Val Gly Glu
20 25 30
Ser Glu Ile Pro Glu Thr Phe Tyr Val Leu Thr Lys
35 40

<210> 111
<211> 932

<212> DNA
<213> Helicobacter pylori
<220>
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<222> (1)..(930)
<400> 111

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tta gcc caa atg cgt tta gcc att gaa gcg gct gaa ggc tct gat ttg   48
Leu Ala Gln Met Arg Leu Ala Ile Glu Ala Ala Glu Gly Ser Asp Leu
 1               5                  10                  15
agc aac gct aac atg ctt ttt aaa gaa gct ttt tct aac gcc aaa gac   96
Ser Asn Ala Asn Met Leu Phe Lys Glu Ala Phe Ser Asn Ala Lys Asp
            20                  25                  30
aaa gag agt gcg agt gaa atc gcg ctt aat tgg gct gaa gca gag ata   144
Lys Glu Ser Ala Ser Glu Ile Ala Leu Asn Trp Ala Glu Ala Glu Ile
        35                  40                  45
aac tat caa aat ttt aat aac gct aaa tac ctc att gat aag gtg gtc   192
Asn Tyr Gln Asn Phe Asn Asn Ala Lys Tyr Leu Ile Asp Lys Val Val
    50                  55                  60
caa tcc aac cct gat tat att tct acg cat agc gaa tca gcc cta gac   240
Gln Ser Asn Pro Asp Tyr Ile Ser Thr His Ser Glu Ser Ala Leu Asp
65                  70                  75                  80
ttg ctc aag tta ttg aaa aaa aac cag atg aat gca agc gcg att gag   288
Leu Leu Lys Leu Leu Lys Lys Asn Gln Met Asn Ala Ser Ala Ile Glu
                85                  90                  95
atc gct cac ttg ctc ctc aat caa gat gat gat ctg aaa gct aaa gag   336
Ile Ala His Leu Leu Leu Asn Gln Asp Asp Asp Leu Lys Ala Lys Glu
            100                 105                 110
caa gcg ctt tat gat tta gga gcg ttg tat gca agg atc aag gac ttt   384
Gln Ala Leu Tyr Asp Leu Gly Ala Leu Tyr Ala Arg Ile Lys Asp Phe
        115                 120                 125
aaa aac gcc cac ctt tac aat ctg caa tat ttg cag gac cat gcg gaa   432
Lys Asn Ala His Leu Tyr Asn Leu Gln Tyr Leu Gln Asp His Ala Glu
    130                 135                 140
ctg gat aaa gct tct gtc gtt agg gcg cgc gat gaa aaa gcc ctt ttt   480
Leu Asp Lys Ala Ser Val Val Arg Ala Arg Asp Glu Lys Ala Leu Phe
145                 150                 155                 160
tcc atg gag ggg aac acg caa gaa aaa atc gcc cac tat gac aaa atc   528
Ser Met Glu Gly Asn Thr Gln Glu Lys Ile Ala His Tyr Asp Lys Ile
                165                 170                 175
att caa aat ttc cct aat tct aat gaa gcc cta aag gct tta gaa ttg   576
Ile Gln Asn Phe Pro Asn Ser Asn Glu Ala Leu Lys Ala Leu Glu Leu
            180                 185                 190
aaa gcc caa cta ttg ttt gaa aac aag cgt tat gct gaa gtg tta agc   624
Lys Ala Gln Leu Leu Phe Glu Asn Lys Arg Tyr Ala Glu Val Leu Ser
        195                 200                 205
atg caa aaa aat ttg cct aaa gat tcc cct ttg atc caa aaa acg ctc   672
Met Gln Lys Asn Leu Pro Lys Asp Ser Pro Leu Ile Gln Lys Thr Leu
    210                 215                 220
aat gtc ctt gct aaa acc cca tta gag aac cat cgt tgt gaa gaa gcc   720
Asn Val Leu Ala Lys Thr Pro Leu Glu Asn His Arg Cys Glu Glu Ala
225                 230                 235                 240
tta aaa tat tta tcc caa atc aca acc ttt gaa ttc agc ccc aaa gaa   768
Leu Lys Tyr Leu Ser Gln Ile Thr Thr Phe Glu Phe Ser Pro Lys Glu
                245                 250                 255
gaa atc caa gcc ttt gat tgc ttg tat ttc gca tcg ctc aaa gaa aaa   816
Glu Ile Gln Ala Phe Asp Cys Leu Tyr Phe Ala Ser Leu Lys Glu Lys
            260                 265                 270
gcg caa atc att gcc cta aac gct ttt aaa acg gct aaa gcc cct agc   864
Ala Gln Ile Ile Ala Leu Asn Ala Phe Lys Thr Ala Lys Ala Pro Ser
        275                 280                 285
gag aaa tta ata tgg ctt tat cgt ttg ggg cgc aat tac tac cgc tta   912
```

```
Glu Lys Leu Ile Trp Leu Tyr Arg Leu Gly Arg Asn Tyr Tyr Arg Leu
    290                 295                 300
ggg gat ttt aaa aat tcc ac                                      932
Gly Asp Phe Lys Asn Ser
305                 310
<210> 112
<211> 310
<212> PRT
<213> Helicobacter pylori
<400> 112
Leu Ala Gln Met Arg Leu Ala Ile Glu Ala Ala Glu Gly Ser Asp Leu
  1               5                  10                  15
Ser Asn Ala Asn Met Leu Phe Lys Glu Ala Phe Ser Asn Ala Lys Asp
            20                  25                  30
Lys Glu Ser Ala Ser Glu Ile Ala Leu Asn Trp Ala Glu Ala Glu Ile
        35                  40                  45
Asn Tyr Gln Asn Phe Asn Asn Ala Lys Tyr Leu Ile Asp Lys Val Val
    50                  55                  60
Gln Ser Asn Pro Asp Tyr Ile Ser Thr His Ser Glu Ser Ala Leu Asp
65                  70                  75                  80
Leu Leu Lys Leu Leu Lys Lys Asn Gln Met Asn Ala Ser Ala Ile Glu
                85                  90                  95
Ile Ala His Leu Leu Leu Asn Gln Asp Asp Asp Leu Lys Ala Lys Glu
            100                 105                 110
Gln Ala Leu Tyr Asp Leu Gly Ala Leu Tyr Ala Arg Ile Lys Asp Phe
        115                 120                 125
Lys Asn Ala His Leu Tyr Asn Leu Gln Tyr Leu Gln Asp His Ala Glu
    130                 135                 140
Leu Asp Lys Ala Ser Val Val Arg Ala Arg Asp Glu Lys Ala Leu Phe
145                 150                 155                 160
Ser Met Glu Gly Asn Thr Gln Glu Lys Ile Ala His Tyr Asp Lys Ile
                165                 170                 175
Ile Gln Asn Phe Pro Asn Ser Asn Glu Ala Leu Lys Ala Leu Glu Leu
            180                 185                 190
Lys Ala Gln Leu Leu Phe Glu Asn Lys Arg Tyr Ala Glu Val Leu Ser
        195                 200                 205
Met Gln Lys Asn Leu Pro Lys Asp Ser Pro Leu Ile Gln Lys Thr Leu
    210                 215                 220
Asn Val Leu Ala Lys Thr Pro Leu Glu Asn His Arg Cys Glu Glu Ala
225                 230                 235                 240
Leu Lys Tyr Leu Ser Gln Ile Thr Thr Phe Glu Phe Ser Pro Lys Glu
                245                 250                 255
Glu Ile Gln Ala Phe Asp Cys Leu Tyr Phe Ala Ser Leu Lys Glu Lys
            260                 265                 270
Ala Gln Ile Ile Ala Leu Asn Ala Phe Lys Thr Ala Lys Ala Pro Ser
        275                 280                 285
Glu Lys Leu Ile Trp Leu Tyr Arg Leu Gly Arg Asn Tyr Tyr Arg Leu
    290                 295                 300
Gly Asp Phe Lys Asn Ser
305                 310
<210> 113
<211> 591
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(591)
<400> 113
gcg aac aaa aag aaa aaa aaa gac gaa tac aac aaa ccg gcg atc ttt   48
Ala Asn Lys Lys Lys Lys Lys Asp Glu Tyr Asn Lys Pro Ala Ile Phe
  1               5                  10                  15
```

```
tgg tat caa ggg att ttg aga gaa atc ctt ttt gct aat tta gaa aca   96
Trp Tyr Gln Gly Ile Leu Arg Glu Ile Leu Phe Ala Asn Leu Glu Thr
            20                  25                  30
gcg gac aat tac tat tct tct tta caa agc gaa cac atc aat tcc ccc   144
Ala Asp Asn Tyr Tyr Ser Ser Leu Gln Ser Glu His Ile Asn Ser Pro
        35                  40                  45
ctt gtc cca gaa gcg atg cta gct tta ggg caa gcg cac atg aaa aag   192
Leu Val Pro Glu Ala Met Leu Ala Leu Gly Gln Ala His Met Lys Lys
    50                  55                  60
aaa gag tat gtt tta gcg tct ttt tac ttt gat gaa tac atc aag cgc   240
Lys Glu Tyr Val Leu Ala Ser Phe Tyr Phe Asp Glu Tyr Ile Lys Arg
65                  70                  75                  80
ttt ggg act aag gac aat gtg gat tat ttg act ttt tta aaa ttg caa   288
Phe Gly Thr Lys Asp Asn Val Asp Tyr Leu Thr Phe Leu Lys Leu Gln
                85                  90                  95
tcg cat tat tac gct ttc aaa aac cat tct aaa gac cag gaa ttt atc   336
Ser His Tyr Tyr Ala Phe Lys Asn His Ser Lys Asp Gln Glu Phe Ile
            100                 105                 110
tct aat tct att gtg agt tta ggc gaa ttt ata gaa aaa tac cct aac   384
Ser Asn Ser Ile Val Ser Leu Gly Glu Phe Ile Glu Lys Tyr Pro Asn
        115                 120                 125
agc cgt tac cgc ccc tat gta gaa tac atg caa atc aaa ttc att tta   432
Ser Arg Tyr Arg Pro Tyr Val Glu Tyr Met Gln Ile Lys Phe Ile Leu
    130                 135                 140
ggg caa aat gag ctc aat cgc gcg atc gcg aat gtc tat aaa aaa cgc   480
Gly Gln Asn Glu Leu Asn Arg Ala Ile Ala Asn Val Tyr Lys Lys Arg
145                 150                 155                 160
cac aag cct gag ggc gtg aaa cgc tat tta gaa agg ata gat gag act   528
His Lys Pro Glu Gly Val Lys Arg Tyr Leu Glu Arg Ile Asp Glu Thr
                165                 170                 175
tta gaa aaa gag act aaa ccc aaa cca tcg cac atg cct tgg tat gtg   576
Leu Glu Lys Glu Thr Lys Pro Lys Pro Ser His Met Pro Trp Tyr Val
            180                 185                 190
tta att ttt gat tgg                                             591
Leu Ile Phe Asp Trp
        195
```

<210> 114
<211> 197
<212> PRT
<213> Helicobacter pylori
<400> 114

```
Ala Asn Lys Lys Lys Lys Lys Asp Glu Tyr Asn Lys Pro Ala Ile Phe
  1               5                  10                  15
Trp Tyr Gln Gly Ile Leu Arg Glu Ile Leu Phe Ala Asn Leu Glu Thr
            20                  25                  30
Ala Asp Asn Tyr Tyr Ser Ser Leu Gln Ser Glu His Ile Asn Ser Pro
        35                  40                  45
Leu Val Pro Glu Ala Met Leu Ala Leu Gly Gln Ala His Met Lys Lys
    50                  55                  60
Lys Glu Tyr Val Leu Ala Ser Phe Tyr Phe Asp Glu Tyr Ile Lys Arg
65                  70                  75                  80
Phe Gly Thr Lys Asp Asn Val Asp Tyr Leu Thr Phe Leu Lys Leu Gln
                85                  90                  95
Ser His Tyr Tyr Ala Phe Lys Asn His Ser Lys Asp Gln Glu Phe Ile
            100                 105                 110
Ser Asn Ser Ile Val Ser Leu Gly Glu Phe Ile Glu Lys Tyr Pro Asn
        115                 120                 125
Ser Arg Tyr Arg Pro Tyr Val Glu Tyr Met Gln Ile Lys Phe Ile Leu
    130                 135                 140
Gly Gln Asn Glu Leu Asn Arg Ala Ile Ala Asn Val Tyr Lys Lys Arg
145                 150                 155                 160
```

His Lys Pro Glu Gly Val Lys Arg Tyr Leu Glu Arg Ile Asp Glu Thr
165 170 175
Leu Glu Lys Glu Thr Lys Pro Lys Pro Ser His Met Pro Trp Tyr Val
180 185 190
Leu Ile Phe Asp Trp
195

<210> 115
<211> 498
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(498)
<400> 115

```
ttt aaa ccc ttt aaa gac gct ttt tac aga gat ttc aat cat aat gag   48
Phe Lys Pro Phe Lys Asp Ala Phe Tyr Arg Asp Phe Asn His Asn Glu
  1               5                  10                  15
caa aag tta ctg ata ggg gca gct aaa agc ggt tgc att caa tct agc   96
Gln Lys Leu Leu Ile Gly Ala Ala Lys Ser Gly Cys Ile Gln Ser Ser
             20                  25                  30
gct gat aaa ctg gct cag tta aaa acg cgc tta ctc tac tgg caa gac  144
Ala Asp Lys Leu Ala Gln Leu Lys Thr Arg Leu Leu Tyr Trp Gln Asp
         35                  40                  45
aaa tct gtt aaa gtg gat tgg gat aaa ccc att tta atc aag gac ttc  192
Lys Ser Val Lys Val Asp Trp Asp Lys Pro Ile Leu Ile Lys Asp Phe
     50                  55                  60
ttt aaa ggc aat aat tac ctt tat agg agg ttt tgt ttt tta ttg ggg  240
Phe Lys Gly Asn Asn Tyr Leu Tyr Arg Arg Phe Cys Phe Leu Leu Gly
 65                  70                  75                  80
aag cat ttt atg gac aga ttt tta aag aat aac gct aag gcg agc gtg  288
Lys His Phe Met Asp Arg Phe Leu Lys Asn Asn Ala Lys Ala Ser Val
                 85                  90                  95
aaa gac ttt atg tct agt aag gag ttt gtc gct aaa tac cga tac acc  336
Lys Asp Phe Met Ser Ser Lys Glu Phe Val Ala Lys Tyr Arg Tyr Thr
            100                 105                 110
ccc aag caa aat aca gaa aga gcg aaa aag ctg caa tcg tat tta gag  384
Pro Lys Gln Asn Thr Glu Arg Ala Lys Lys Leu Gln Ser Tyr Leu Glu
        115                 120                 125
aat aag cgc gat ttt ata ggg ttt gtt caa gcg ctt aac tct tta aaa  432
Asn Lys Arg Asp Phe Ile Gly Phe Val Gln Ala Leu Asn Ser Leu Lys
    130                 135                 140
gac aac ccg caa gat cct ttt tta ccc aat gaa gaa acg agc ttt ttg  480
Asp Asn Pro Gln Asp Pro Phe Leu Pro Asn Glu Glu Thr Ser Phe Leu
145                 150                 155                 160
gtg ttc gct aat gag cct                                         498
Val Phe Ala Asn Glu Pro
                165
```

<210> 116
<211> 166
<212> PRT
<213> Helicobacter pylori
<400> 116

```
Phe Lys Pro Phe Lys Asp Ala Phe Tyr Arg Asp Phe Asn His Asn Glu
  1               5                  10                  15
Gln Lys Leu Leu Ile Gly Ala Ala Lys Ser Gly Cys Ile Gln Ser Ser
             20                  25                  30
Ala Asp Lys Leu Ala Gln Leu Lys Thr Arg Leu Leu Tyr Trp Gln Asp
         35                  40                  45
Lys Ser Val Lys Val Asp Trp Asp Lys Pro Ile Leu Ile Lys Asp Phe
     50                  55                  60
Phe Lys Gly Asn Asn Tyr Leu Tyr Arg Arg Phe Cys Phe Leu Leu Gly
```

```
 65                  70                  75                  80
Lys His Phe Met Asp Arg Phe Leu Lys Asn Asn Ala Lys Ala Ser Val
                 85                  90                  95
Lys Asp Phe Met Ser Ser Lys Glu Phe Val Ala Lys Tyr Arg Tyr Thr
            100                 105                 110
Pro Lys Gln Asn Thr Glu Arg Ala Lys Lys Leu Gln Ser Tyr Leu Glu
        115                 120                 125
Asn Lys Arg Asp Phe Ile Gly Phe Val Gln Ala Leu Asn Ser Leu Lys
    130                 135                 140
Asp Asn Pro Gln Asp Pro Phe Leu Pro Asn Glu Glu Thr Ser Phe Leu
145                 150                 155                 160
Val Phe Ala Asn Glu Pro
                165
```

<210> 117
<211> 399
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(399)
<400> 117

```
ctc gct ttg aat gag ttg aat ccg ggc gaa tgg gtg gtg cat gat gat   48
Leu Ala Leu Asn Glu Leu Asn Pro Gly Glu Trp Val Val His Asp Asp
  1               5                  10                  15
tat ggg gtg ggc gtg ttt tct caa tta gtc cag cac agc gtt tta ggg   96
Tyr Gly Val Gly Val Phe Ser Gln Leu Val Gln His Ser Val Leu Gly
             20                  25                  30
agc aag agg gat ttt tta gaa atc gct tat ttg ggc gaa gac aaa ctg   144
Ser Lys Arg Asp Phe Leu Glu Ile Ala Tyr Leu Gly Glu Asp Lys Leu
         35                  40                  45
ctg tta ccg gta gaa aac ttg cat ctc atc gct cgc tat gtg gcg caa   192
Leu Leu Pro Val Glu Asn Leu His Leu Ile Ala Arg Tyr Val Ala Gln
     50                  55                  60
agc gat agc gtg cca gct aaa gac cgg cta ggg aaa ggg agc ttt ctt   240
Ser Asp Ser Val Pro Ala Lys Asp Arg Leu Gly Lys Gly Ser Phe Leu
 65                  70                  75                  80
aaa tta aaa gct aaa gtc agg act aag ctt tta gag att gct agc aag   288
Lys Leu Lys Ala Lys Val Arg Thr Lys Leu Leu Glu Ile Ala Ser Lys
                 85                  90                  95
atc att gaa tta gcg gct gaa cgc aat ttg atc ttg ggt aaa aag atg   336
Ile Ile Glu Leu Ala Ala Glu Arg Asn Leu Ile Leu Gly Lys Lys Met
            100                 105                 110
gat gtg cat tta gcg gag ttg gaa gtc ttt aaa tcg cat gcg ggg ttt   384
Asp Val His Leu Ala Glu Leu Glu Val Phe Lys Ser His Ala Gly Phe
        115                 120                 125
gaa tac acc agc gat                                             399
Glu Tyr Thr Ser Asp
    130
```

<210> 118
<211> 133
<212> PRT
<213> Helicobacter pylori
<400> 118

```
Leu Ala Leu Asn Glu Leu Asn Pro Gly Glu Trp Val Val His Asp Asp
  1               5                  10                  15
Tyr Gly Val Gly Val Phe Ser Gln Leu Val Gln His Ser Val Leu Gly
             20                  25                  30
Ser Lys Arg Asp Phe Leu Glu Ile Ala Tyr Leu Gly Glu Asp Lys Leu
         35                  40                  45
Leu Leu Pro Val Glu Asn Leu His Leu Ile Ala Arg Tyr Val Ala Gln
     50                  55                  60
```

```
Ser Asp Ser Val Pro Ala Lys Asp Arg Leu Gly Lys Gly Ser Phe Leu
 65                  70                  75                  80
Lys Leu Lys Ala Lys Val Arg Thr Lys Leu Leu Glu Ile Ala Ser Lys
                 85                  90                  95
Ile Ile Glu Leu Ala Ala Glu Arg Asn Leu Ile Leu Gly Lys Lys Met
            100                 105                 110
Asp Val His Leu Ala Glu Leu Glu Val Phe Lys Ser His Ala Gly Phe
        115                 120                 125
Glu Tyr Thr Ser Asp
    130
<210> 119
<211> 426
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(426)
<400> 119
gtt tta aac gca ccc atc act tta gaa gac att caa gaa tta agc tcc   48
Val Leu Asn Ala Pro Ile Thr Leu Glu Asp Ile Gln Glu Leu Ser Ser
  1               5                  10                  15
aat gcg ggg gat atg gat ttg caa aag ctc att tta ggg ctt ttt tta   96
Asn Ala Gly Asp Met Asp Leu Gln Lys Leu Ile Leu Gly Leu Phe Leu
            20                  25                  30
aaa aaa agt gcg ctt gat att tat gat tat ttg tta aaa gag ggc aaa   144
Lys Lys Ser Ala Leu Asp Ile Tyr Asp Tyr Leu Leu Lys Glu Gly Lys
        35                  40                  45
aaa gat gcg gat att tta agg ggg tta gag cgc tat ttt tac caa ctt   192
Lys Asp Ala Asp Ile Leu Arg Gly Leu Glu Arg Tyr Phe Tyr Gln Leu
    50                  55                  60
ttt tta ttt ttc gct cat att aaa acg acc ggt tta atg gac gct aaa   240
Phe Leu Phe Phe Ala His Ile Lys Thr Thr Gly Leu Met Asp Ala Lys
65                  70                  75                  80
gag gtt tta ggc tac gct ccc cct aaa gaa att gcc gaa aat tac gct   288
Glu Val Leu Gly Tyr Ala Pro Pro Lys Glu Ile Ala Glu Asn Tyr Ala
                85                  90                  95
aaa aac gcc ttg cgt ttg aaa gaa gcc ggc tat aag agg gtt ttt gaa   336
Lys Asn Ala Leu Arg Leu Lys Glu Ala Gly Tyr Lys Arg Val Phe Glu
            100                 105                 110
att ttt agg tta tgg cac att caa agc atg caa ggg caa aag gaa ttg   384
Ile Phe Arg Leu Trp His Ile Gln Ser Met Gln Gly Gln Lys Glu Leu
        115                 120                 125
ggc ttt ttg tat ttg acc tcc att caa aaa atc att aac ccc           426
Gly Phe Leu Tyr Leu Thr Ser Ile Gln Lys Ile Ile Asn Pro
    130                 135                 140
<210> 120
<211> 142
<212> PRT
<213> Helicobacter pylori
<400> 120
Val Leu Asn Ala Pro Ile Thr Leu Glu Asp Ile Gln Glu Leu Ser Ser
  1               5                  10                  15
Asn Ala Gly Asp Met Asp Leu Gln Lys Leu Ile Leu Gly Leu Phe Leu
            20                  25                  30
Lys Lys Ser Ala Leu Asp Ile Tyr Asp Tyr Leu Leu Lys Glu Gly Lys
        35                  40                  45
Lys Asp Ala Asp Ile Leu Arg Gly Leu Glu Arg Tyr Phe Tyr Gln Leu
    50                  55                  60
Phe Leu Phe Phe Ala His Ile Lys Thr Thr Gly Leu Met Asp Ala Lys
65                  70                  75                  80
Glu Val Leu Gly Tyr Ala Pro Pro Lys Glu Ile Ala Glu Asn Tyr Ala
```

```
                85                  90                  95
Lys Asn Ala Leu Arg Leu Lys Glu Ala Gly Tyr Lys Arg Val Phe Glu
            100                 105                 110
Ile Phe Arg Leu Trp His Ile Gln Ser Met Gln Gly Gln Lys Glu Leu
        115                 120                 125
Gly Phe Leu Tyr Leu Thr Ser Ile Gln Lys Ile Ile Asn Pro
    130                 135                 140
<210> 121
<211> 297
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(297)
<400> 121
gaa gaa tgc ggc acg ctt tta gaa ttg agg gaa aaa att tcg ttg ttt   48
Glu Glu Cys Gly Thr Leu Leu Glu Leu Arg Glu Lys Ile Ser Leu Phe
  1               5                  10                  15
tta gag cca aag gat att gtt aaa act tat gaa aat gaa gat ttt aaa   96
Leu Glu Pro Lys Asp Ile Val Lys Thr Tyr Glu Asn Glu Asp Phe Lys
            20                  25                  30
gag cgt tgt tta gcg ctt ttt aac gct cta aca agc atg gat ttt caa   144
Glu Arg Cys Leu Ala Leu Phe Asn Ala Leu Thr Ser Met Asp Phe Gln
        35                  40                  45
gcg tat aag gat ttt gaa agt ttt aaa aaa gaa gcc atg cga tta agc   192
Ala Tyr Lys Asp Phe Glu Ser Phe Lys Lys Glu Ala Met Arg Leu Ser
    50                  55                  60
cag ctt aag ggt aag gat ttt ttc aaa cct ttg cgc atc ctt tta acc   240
Gln Leu Lys Gly Lys Asp Phe Phe Lys Pro Leu Arg Ile Leu Leu Thr
65                  70                  75                  80
ggg aac tcg cat ggc gtt gaa ttg cct ttg att ttc ccc tat atc caa   288
Gly Asn Ser His Gly Val Glu Leu Pro Leu Ile Phe Pro Tyr Ile Gln
                85                  90                  95
agc cat cat                                                      297
Ser His His
<210> 122
<211> 99
<212> PRT
<213> Helicobacter pylori
<400> 122
Glu Glu Cys Gly Thr Leu Leu Glu Leu Arg Glu Lys Ile Ser Leu Phe
  1               5                  10                  15
Leu Glu Pro Lys Asp Ile Val Lys Thr Tyr Glu Asn Glu Asp Phe Lys
            20                  25                  30
Glu Arg Cys Leu Ala Leu Phe Asn Ala Leu Thr Ser Met Asp Phe Gln
        35                  40                  45
Ala Tyr Lys Asp Phe Glu Ser Phe Lys Lys Glu Ala Met Arg Leu Ser
    50                  55                  60
Gln Leu Lys Gly Lys Asp Phe Phe Lys Pro Leu Arg Ile Leu Leu Thr
65                  70                  75                  80
Gly Asn Ser His Gly Val Glu Leu Pro Leu Ile Phe Pro Tyr Ile Gln
                85                  90                  95
Ser His His
<210> 123
<211> 42
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(42)
<400> 123
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```
ccc caa atc gta gct aaa gat ttt tta gaa aga tta ggg tta           42
Pro Gln Ile Val Ala Lys Asp Phe Leu Glu Arg Leu Gly Leu
 1               5                  10
<210> 124
<211> 14
<212> PRT
<213> Helicobacter pylori
<400> 124
Pro Gln Ile Val Ala Lys Asp Phe Leu Glu Arg Leu Gly Leu
 1               5                  10
<210> 125
<211> 84
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(84)
<400> 125
aag aaa gcg att gaa aat aac cag tat aaa atc aac ttg cat gag act   48
Lys Lys Ala Ile Glu Asn Asn Gln Tyr Lys Ile Asn Leu His Glu Thr
 1               5                  10                  15
tct cac aaa atg gca aag gat tta ttg ggg ata agc                   84
Ser His Lys Met Ala Lys Asp Leu Leu Gly Ile Ser
            20                  25
<210> 126
<211> 28
<212> PRT
<213> Helicobacter pylori
<400> 126
Lys Lys Ala Ile Glu Asn Asn Gln Tyr Lys Ile Asn Leu His Glu Thr
 1               5                  10                  15
Ser His Lys Met Ala Lys Asp Leu Leu Gly Ile Ser
            20                  25
<210> 127
<211> 356
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(354)
<400> 127
cac att tat gaa aaa gaa gtg gat gct agg gag ctt aag cat ggt gtg   48
His Ile Tyr Glu Lys Glu Val Asp Ala Arg Glu Leu Lys His Gly Val
 1               5                  10                  15
gaa gaa ttt acc gct gat att cct gat gtg aaa gaa gaa gcg ctc gct   96
Glu Glu Phe Thr Ala Asp Ile Pro Asp Val Lys Glu Glu Ala Leu Ala
            20                  25                  30
cat ctt gat gaa agc ggg atc gtt aaa gtc ggt act tat gtg agc gct  144
His Leu Asp Glu Ser Gly Ile Val Lys Val Gly Thr Tyr Val Ser Ala
        35                  40                  45
ggc atg att ttg gtg ggc aaa act tct cct aaa ggc gag att aaa agc  192
Gly Met Ile Leu Val Gly Lys Thr Ser Pro Lys Gly Glu Ile Lys Ser
    50                  55                  60
acg cct gaa gag cgg ctt tta agg gct att ttt ggg gat aaa gcc ggg  240
Thr Pro Glu Glu Arg Leu Leu Arg Ala Ile Phe Gly Asp Lys Ala Gly
65                  70                  75                  80
cat gtg gtc aat aag agt ttg tat tgc cct ccc agt ttg gaa ggc acg  288
His Val Val Asn Lys Ser Leu Tyr Cys Pro Pro Ser Leu Glu Gly Thr
                85                  90                  95
gtg att gat gtg aaa gtc ttc act aaa aaa ggc tat gag aaa gac gcg  336
Val Ile Asp Val Lys Val Phe Thr Lys Lys Gly Tyr Glu Lys Asp Ala
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100 105 110
cga gtt ttg agc gcg tat ga 356
Arg Val Leu Ser Ala Tyr
115

<210> 128
<211> 118
<212> PRT
<213> Helicobacter pylori
<400> 128
His Ile Tyr Glu Lys Glu Val Asp Ala Arg Glu Leu Lys His Gly Val
1 5 10 15
Glu Glu Phe Thr Ala Asp Ile Pro Asp Val Lys Glu Glu Ala Leu Ala
20 25 30
His Leu Asp Glu Ser Gly Ile Val Lys Val Gly Thr Tyr Val Ser Ala
35 40 45
Gly Met Ile Leu Val Gly Lys Thr Ser Pro Lys Gly Glu Ile Lys Ser
50 55 60
Thr Pro Glu Glu Arg Leu Leu Arg Ala Ile Phe Gly Asp Lys Ala Gly
65 70 75 80
His Val Val Asn Lys Ser Leu Tyr Cys Pro Pro Ser Leu Glu Gly Thr
85 90 95
Val Ile Asp Val Lys Val Phe Thr Lys Lys Gly Tyr Glu Lys Asp Ala
100 105 110
Arg Val Leu Ser Ala Tyr
115

<210> 129
<211> 698
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(696)
<400> 129
tat aag ccc tac acc cca agc aga cgc ttc atg tcg gtg ttg gac tct 48
Tyr Lys Pro Tyr Thr Pro Ser Arg Arg Phe Met Ser Val Leu Asp Ser
1 5 10 15
aaa gac att acc gca aaa agc agt gtc aaa ggc tta ctc act aag ctt 96
Lys Asp Ile Thr Ala Lys Ser Ser Val Lys Gly Leu Leu Thr Lys Leu
20 25 30
aaa gca aca gca ggg aga aac aat aac ggg cgc atc acc agc cgc cac 144
Lys Ala Thr Ala Gly Arg Asn Asn Asn Gly Arg Ile Thr Ser Arg His
35 40 45
aaa gag aga ggg gct aaa aaa ctc tat cgc att att gat ttc aag cgc 192
Lys Glu Arg Gly Ala Lys Lys Leu Tyr Arg Ile Ile Asp Phe Lys Arg
50 55 60
aat aaa tac aat att gaa ggg aaa gtg gct gcg att gag tat gat cct 240
Asn Lys Tyr Asn Ile Glu Gly Lys Val Ala Ala Ile Glu Tyr Asp Pro
65 70 75 80
tac aga aat gcg cgc atc gct ctt gta gtc tat cct gat ggg gac aaa 288
Tyr Arg Asn Ala Arg Ile Ala Leu Val Val Tyr Pro Asp Gly Asp Lys
85 90 95
cgc tat att tta cag cca agc ggt ttg aaa gtg ggc gat agc gtt atc 336
Arg Tyr Ile Leu Gln Pro Ser Gly Leu Lys Val Gly Asp Ser Val Ile
100 105 110
gct gct gaa ggc ggt ttg gat att aaa gtg ggc ttt gcg atg aag tta 384
Ala Ala Glu Gly Gly Leu Asp Ile Lys Val Gly Phe Ala Met Lys Leu
115 120 125
aaa aat atc ccc ata gga acg gtg gtg cat aat att gaa atg cat cca 432
Lys Asn Ile Pro Ile Gly Thr Val Val His Asn Ile Glu Met His Pro
130 135 140
ggg gct ggc ggg caa tta gcc aga agc gca gga atg agc gct caa atc 480

```
Gly Ala Gly Gly Gln Leu Ala Arg Ser Ala Gly Met Ser Ala Gln Ile
145                 150                 155                 160
atg ggt aga gaa aat aaa tac acc att att agg atg cca agc tct gaa   528
Met Gly Arg Glu Asn Lys Tyr Thr Ile Ile Arg Met Pro Ser Ser Glu
                165                 170                 175
atg cgc tac att cta agc gaa tgt atg gcg agt gtt ggc gtg gta ggg   576
Met Arg Tyr Ile Leu Ser Glu Cys Met Ala Ser Val Gly Val Val Gly
            180                 185                 190
aat gag gat ttt atc aat gtc tct atc ggt aag gca ggg cgt aac cgc   624
Asn Glu Asp Phe Ile Asn Val Ser Ile Gly Lys Ala Gly Arg Asn Arg
        195                 200                 205
cac aga ggg atc cgc cca caa act cgt ggt agc gcg atg aac cca gtg   672
His Arg Gly Ile Arg Pro Gln Thr Arg Gly Ser Ala Met Asn Pro Val
    210                 215                 220
gat cac ccg cat ggt ggg ggt gag gg                               698
Asp His Pro His Gly Gly Gly Glu
225                 230
<210> 130
<211> 232
<212> PRT
<213> Helicobacter pylori
<400> 130
Tyr Lys Pro Tyr Thr Pro Ser Arg Arg Phe Met Ser Val Leu Asp Ser
  1               5                  10                  15
Lys Asp Ile Thr Ala Lys Ser Ser Val Lys Gly Leu Leu Thr Lys Leu
             20                  25                  30
Lys Ala Thr Ala Gly Arg Asn Asn Asn Gly Arg Ile Thr Ser Arg His
         35                  40                  45
Lys Glu Arg Gly Ala Lys Lys Leu Tyr Arg Ile Ile Asp Phe Lys Arg
     50                  55                  60
Asn Lys Tyr Asn Ile Glu Gly Lys Val Ala Ala Ile Glu Tyr Asp Pro
 65                  70                  75                  80
Tyr Arg Asn Ala Arg Ile Ala Leu Val Val Tyr Pro Asp Gly Asp Lys
                 85                  90                  95
Arg Tyr Ile Leu Gln Pro Ser Gly Leu Lys Val Gly Asp Ser Val Ile
            100                 105                 110
Ala Ala Glu Gly Gly Leu Asp Ile Lys Val Gly Phe Ala Met Lys Leu
        115                 120                 125
Lys Asn Ile Pro Ile Gly Thr Val Val His Asn Ile Glu Met His Pro
    130                 135                 140
Gly Ala Gly Gly Gln Leu Ala Arg Ser Ala Gly Met Ser Ala Gln Ile
145                 150                 155                 160
Met Gly Arg Glu Asn Lys Tyr Thr Ile Ile Arg Met Pro Ser Ser Glu
                165                 170                 175
Met Arg Tyr Ile Leu Ser Glu Cys Met Ala Ser Val Gly Val Val Gly
            180                 185                 190
Asn Glu Asp Phe Ile Asn Val Ser Ile Gly Lys Ala Gly Arg Asn Arg
        195                 200                 205
His Arg Gly Ile Arg Pro Gln Thr Arg Gly Ser Ala Met Asn Pro Val
    210                 215                 220
Asp His Pro His Gly Gly Gly Glu
225                 230
<210> 131
<211> 528
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(528)
<400> 131
tac gat tgg atc aag gaa ttt gtg cgc gat caa gga gag ttt atc gcc   48
```

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Tyr Asp Trp Ile Lys Glu Phe Val Arg Asp Gln Gly Glu Phe Ile Ala
 1               5                  10                  15
caa caa agc ggg tgg ctg gaa tta gag cga tca agc tat gcc aaa ctc   96
Gln Gln Ser Gly Trp Leu Glu Leu Glu Arg Ser Ser Tyr Ala Lys Leu
            20                  25                  30
atc gcg caa acc atc tcg cat gtg ctt aat ggc gga tcg ctg ttg gtg   144
Ile Ala Gln Thr Ile Ser His Val Leu Asn Gly Gly Ser Leu Leu Val
        35                  40                  45
agc gcg gat tct tct agg cac tgg ttt tta aac tac att ctt tct aac   192
Ser Ala Asp Ser Ser Arg His Trp Phe Leu Asn Tyr Ile Leu Ser Asn
    50                  55                  60
cta aac ccc aaa gat tta aaa gag cgc ccc tta ttg tcc gtc att gat   240
Leu Asn Pro Lys Asp Leu Lys Glu Arg Pro Leu Leu Ser Val Ile Asp
65                  70                  75                  80
ttt aac gct tct tct ttc tac ccc aaa aac gat gcg aat ctc tct cta   288
Phe Asn Ala Ser Ser Phe Tyr Pro Lys Asn Asp Ala Asn Leu Ser Leu
                85                  90                  95
gcc acc ata gag atg act tat caa aac ccc atg ttt tgg cat gtt ggg   336
Ala Thr Ile Glu Met Thr Tyr Gln Asn Pro Met Phe Trp His Val Gly
            100                 105                 110
aaa att gaa aat gaa ggc tta aaa acg ata cta ttg agt aaa atc cct   384
Lys Ile Glu Asn Glu Gly Leu Lys Thr Ile Leu Leu Ser Lys Ile Pro
        115                 120                 125
agt ttt tta tgg ctt ttt gaa gag ctt aaa gaa gat tgc ttg ctt tta   432
Ser Phe Leu Trp Leu Phe Glu Glu Leu Lys Glu Asp Cys Leu Leu Leu
    130                 135                 140
aaa gag cat gac agc ttg ctg gat tat aaa tta ttg cag ctc ttc aaa   480
Lys Glu His Asp Ser Leu Leu Asp Tyr Lys Leu Leu Gln Leu Phe Lys
145                 150                 155                 160
ctc ttt gaa aac gcg ctt ttt agc gtg cta tac aat aag gtt act ctg   528
Leu Phe Glu Asn Ala Leu Phe Ser Val Leu Tyr Asn Lys Val Thr Leu
                165                 170                 175
```

<210> 132
<211> 176
<212> PRT
<213> Helicobacter pylori
<400> 132

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Tyr Asp Trp Ile Lys Glu Phe Val Arg Asp Gln Gly Glu Phe Ile Ala
 1               5                  10                  15
Gln Gln Ser Gly Trp Leu Glu Leu Glu Arg Ser Ser Tyr Ala Lys Leu
            20                  25                  30
Ile Ala Gln Thr Ile Ser His Val Leu Asn Gly Gly Ser Leu Leu Val
        35                  40                  45
Ser Ala Asp Ser Ser Arg His Trp Phe Leu Asn Tyr Ile Leu Ser Asn
    50                  55                  60
Leu Asn Pro Lys Asp Leu Lys Glu Arg Pro Leu Leu Ser Val Ile Asp
65                  70                  75                  80
Phe Asn Ala Ser Ser Phe Tyr Pro Lys Asn Asp Ala Asn Leu Ser Leu
                85                  90                  95
Ala Thr Ile Glu Met Thr Tyr Gln Asn Pro Met Phe Trp His Val Gly
            100                 105                 110
Lys Ile Glu Asn Glu Gly Leu Lys Thr Ile Leu Leu Ser Lys Ile Pro
        115                 120                 125
Ser Phe Leu Trp Leu Phe Glu Glu Leu Lys Glu Asp Cys Leu Leu Leu
    130                 135                 140
Lys Glu His Asp Ser Leu Leu Asp Tyr Lys Leu Leu Gln Leu Phe Lys
145                 150                 155                 160
Leu Phe Glu Asn Ala Leu Phe Ser Val Leu Tyr Asn Lys Val Thr Leu
                165                 170                 175
```

<210> 133
<211> 263

<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(261)
<400> 133
ttg gcg cta gtc aaa caa aat cct aaa gtt agt ctc ata gag tat gaa 48
Leu Ala Leu Val Lys Gln Asn Pro Lys Val Ser Leu Ile Glu Tyr Glu
1 5 10 15
aat tac ttt agc caa ctc aaa tac aac cct aac gca agc aag agc gat 96
Asn Tyr Phe Ser Gln Leu Lys Tyr Asn Pro Asn Ala Ser Lys Ser Asp
20 25 30
att gcc ttt ttt tat gcc ccc aac caa gtc tta tgc acc acg att aca 144
Ile Ala Phe Phe Tyr Ala Pro Asn Gln Val Leu Cys Thr Thr Ile Thr
35 40 45
gct aaa tac ggc gcg ttg ctt aaa gaa att tta agc cag aat aaa gtc 192
Ala Lys Tyr Gly Ala Leu Leu Lys Glu Ile Leu Ser Gln Asn Lys Val
50 55 60
ggc atg cat tta gcc cac agc gtg gat gtg cgt att gaa gta gcg cct 240
Gly Met His Leu Ala His Ser Val Asp Val Arg Ile Glu Val Ala Pro
65 70 75 80
aaa atc caa att aac gcc caa tc 263
Lys Ile Gln Ile Asn Ala Gln
85

<210> 134
<211> 87
<212> PRT
<213> Helicobacter pylori
<400> 134
Leu Ala Leu Val Lys Gln Asn Pro Lys Val Ser Leu Ile Glu Tyr Glu
1 5 10 15
Asn Tyr Phe Ser Gln Leu Lys Tyr Asn Pro Asn Ala Ser Lys Ser Asp
20 25 30
Ile Ala Phe Phe Tyr Ala Pro Asn Gln Val Leu Cys Thr Thr Ile Thr
35 40 45
Ala Lys Tyr Gly Ala Leu Leu Lys Glu Ile Leu Ser Gln Asn Lys Val
50 55 60
Gly Met His Leu Ala His Ser Val Asp Val Arg Ile Glu Val Ala Pro
65 70 75 80
Lys Ile Gln Ile Asn Ala Gln
85

<210> 135
<211> 447
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(447)
<400> 135
agc tat gcc aaa ctc atc gcg caa acc atc tcg cat gtg ctt aat ggc 48
Ser Tyr Ala Lys Leu Ile Ala Gln Thr Ile Ser His Val Leu Asn Gly
1 5 10 15
gga tcg ctg ttg gtg agc gcg gat tct tct agg cac tgg ttt tta aac 96
Gly Ser Leu Leu Val Ser Ala Asp Ser Ser Arg His Trp Phe Leu Asn
20 25 30
tac att ctt tct aac cta aac ccc aaa gat tta aaa gag cgc ccc tta 144
Tyr Ile Leu Ser Asn Leu Asn Pro Lys Asp Leu Lys Glu Arg Pro Leu
35 40 45
ttg tcc gtc att gat ttt aac gct tct tct ttc tac ccc aaa aac gat 192
Leu Ser Val Ile Asp Phe Asn Ala Ser Ser Phe Tyr Pro Lys Asn Asp
50 55 60

```
gcg aat ctc tct cta gcc acc ata gag atg act tat caa aac ccc atg   240
Ala Asn Leu Ser Leu Ala Thr Ile Glu Met Thr Tyr Gln Asn Pro Met
 65                  70                  75                  80
ttt tgg cat gtt ggg aaa att gaa aat gaa ggc tta aaa acg ata cta   288
Phe Trp His Val Gly Lys Ile Glu Asn Glu Gly Leu Lys Thr Ile Leu
                85                  90                  95
ttg agt aaa atc cct agt ttt tta tgg ctt ttt gaa gag ctt aaa gaa   336
Leu Ser Lys Ile Pro Ser Phe Leu Trp Leu Phe Glu Glu Leu Lys Glu
            100                 105                 110
gat tgc ttg ctt tta aaa gag cat gac agc ttg ctg gat tat aaa tta   384
Asp Cys Leu Leu Leu Lys Glu His Asp Ser Leu Leu Asp Tyr Lys Leu
        115                 120                 125
ttg cag ctc ttc aaa ctc ttt gaa aac gcg ctt ttt agc gtg cta tac   432
Leu Gln Leu Phe Lys Leu Phe Glu Asn Ala Leu Phe Ser Val Leu Tyr
    130                 135                 140
aat aag gtt act ctg                                           447
Asn Lys Val Thr Leu
145
<210> 136
<211> 149
<212> PRT
<213> Helicobacter pylori
<400> 136
Ser Tyr Ala Lys Leu Ile Ala Gln Thr Ile Ser His Val Leu Asn Gly
  1               5                  10                  15
Gly Ser Leu Leu Val Ser Ala Asp Ser Ser Arg His Trp Phe Leu Asn
            20                  25                  30
Tyr Ile Leu Ser Asn Leu Asn Pro Lys Asp Leu Lys Glu Arg Pro Leu
        35                  40                  45
Leu Ser Val Ile Asp Phe Asn Ala Ser Ser Phe Tyr Pro Lys Asn Asp
    50                  55                  60
Ala Asn Leu Ser Leu Ala Thr Ile Glu Met Thr Tyr Gln Asn Pro Met
 65                  70                  75                  80
Phe Trp His Val Gly Lys Ile Glu Asn Glu Gly Leu Lys Thr Ile Leu
                85                  90                  95
Leu Ser Lys Ile Pro Ser Phe Leu Trp Leu Phe Glu Glu Leu Lys Glu
            100                 105                 110
Asp Cys Leu Leu Leu Lys Glu His Asp Ser Leu Leu Asp Tyr Lys Leu
        115                 120                 125
Leu Gln Leu Phe Lys Leu Phe Glu Asn Ala Leu Phe Ser Val Leu Tyr
    130                 135                 140
Asn Lys Val Thr Leu
145
<210> 137
<211> 795
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(795)
<400> 137
gga ctt gga gga ggg act ggg act gga gcc acc cct act atc gtt aaa    48
Gly Leu Gly Gly Gly Thr Gly Thr Gly Ala Thr Pro Thr Ile Val Lys
  1               5                  10                  15
atc gca aaa gaa gtg gga gcg ctc acg att gct atc gtt acc aag cct    96
Ile Ala Lys Glu Val Gly Ala Leu Thr Ile Ala Ile Val Thr Lys Pro
            20                  25                  30
ttc aaa tac gaa ggg aat caa aaa aga aag agg gct gaa gag gga ttg   144
Phe Lys Tyr Glu Gly Asn Gln Lys Arg Lys Arg Ala Glu Glu Gly Leu
        35                  40                  45
aaa gaa ttg gag cag tct agc gat tct att ttg gtt atc cct aat gac   192
```

```
Lys Glu Leu Glu Gln Ser Ser Asp Ser Ile Leu Val Ile Pro Asn Asp
     50                  55                  60
aaa atc ctt ctc acc atg aaa aaa aac gct agc acc acg gag tgt tat   240
Lys Ile Leu Leu Thr Met Lys Lys Asn Ala Ser Thr Thr Glu Cys Tyr
 65                  70                  75                  80
agg gaa gtt gat gat gtc ttg gtt agg gct gtg agt ggc att tct act   288
Arg Glu Val Asp Asp Val Leu Val Arg Ala Val Ser Gly Ile Ser Thr
                 85                  90                  95
atc atc act aaa ccc ggt aat atc aat gtt gat ttt gcc gat tta aag   336
Ile Ile Thr Lys Pro Gly Asn Ile Asn Val Asp Phe Ala Asp Leu Lys
            100                 105                 110
agc gct ctt ggt ttt aaa ggc ttt gcg tta atg ggt att ggt gaa gcc   384
Ser Ala Leu Gly Phe Lys Gly Phe Ala Leu Met Gly Ile Gly Glu Ala
        115                 120                 125
act ggc gaa gaa tcc gct aaa tta gcg gtg caa aat gcg atc caa tcg   432
Thr Gly Glu Glu Ser Ala Lys Leu Ala Val Gln Asn Ala Ile Gln Ser
    130                 135                 140
cct ctt ctt gat gac gct tct att gaa ggg gct aag agc att att gtc   480
Pro Leu Leu Asp Asp Ala Ser Ile Glu Gly Ala Lys Ser Ile Ile Val
145                 150                 155                 160
ttt ttt gag cac cac cct gat tat cct atg atg gct tat tct caa gcg   528
Phe Phe Glu His His Pro Asp Tyr Pro Met Met Ala Tyr Ser Gln Ala
                165                 170                 175
tgc gat ttt att caa gat caa gcc cat caa gat gtt gac gtt aag ttt   576
Cys Asp Phe Ile Gln Asp Gln Ala His Gln Asp Val Asp Val Lys Phe
            180                 185                 190
ggc caa cac acg agc gat aat atc cct att gat cat gtg cgc gtt act   624
Gly Gln His Thr Ser Asp Asn Ile Pro Ile Asp His Val Arg Val Thr
        195                 200                 205
atc att gca acc ggt gct gaa aga aac agc ggt gga gcg agt ttg gaa   672
Ile Ile Ala Thr Gly Ala Glu Arg Asn Ser Gly Gly Ala Ser Leu Glu
    210                 215                 220
tct atc gct acg ccc tct cag cct gtg gtg aaa caa acg aga aaa gtg   720
Ser Ile Ala Thr Pro Ser Gln Pro Val Val Lys Gln Thr Arg Lys Val
225                 230                 235                 240
ggt aat ggc gag tat tta aag atc cct act gaa gaa gag cta tcc ata   768
Gly Asn Gly Glu Tyr Leu Lys Ile Pro Thr Glu Glu Glu Leu Ser Ile
                245                 250                 255
ccc aca acc atg aga atc cag caa gac                              795
Pro Thr Thr Met Arg Ile Gln Gln Asp
            260                 265
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<210> 138
<211> 265
<212> PRT
<213> Helicobacter pylori
<400> 138

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Gly Leu Gly Gly Gly Thr Gly Thr Gly Ala Thr Pro Thr Ile Val Lys
  1               5                  10                  15
Ile Ala Lys Glu Val Gly Ala Leu Thr Ile Ala Ile Val Thr Lys Pro
            20                  25                  30
Phe Lys Tyr Glu Gly Asn Gln Lys Arg Lys Arg Ala Glu Glu Gly Leu
        35                  40                  45
Lys Glu Leu Glu Gln Ser Ser Asp Ser Ile Leu Val Ile Pro Asn Asp
    50                  55                  60
Lys Ile Leu Leu Thr Met Lys Lys Asn Ala Ser Thr Thr Glu Cys Tyr
65                  70                  75                  80
Arg Glu Val Asp Asp Val Leu Val Arg Ala Val Ser Gly Ile Ser Thr
                85                  90                  95
Ile Ile Thr Lys Pro Gly Asn Ile Asn Val Asp Phe Ala Asp Leu Lys
            100                 105                 110
Ser Ala Leu Gly Phe Lys Gly Phe Ala Leu Met Gly Ile Gly Glu Ala
```

```
      115                 120                 125
Thr Gly Glu Glu Ser Ala Lys Leu Ala Val Gln Asn Ala Ile Gln Ser
    130                 135                 140
Pro Leu Leu Asp Asp Ala Ser Ile Glu Gly Ala Lys Ser Ile Ile Val
145                 150                 155                 160
Phe Phe Glu His His Pro Asp Tyr Pro Met Met Ala Tyr Ser Gln Ala
                165                 170                 175
Cys Asp Phe Ile Gln Asp Gln Ala His Gln Asp Val Asp Val Lys Phe
            180                 185                 190
Gly Gln His Thr Ser Asp Asn Ile Pro Ile Asp His Val Arg Val Thr
        195                 200                 205
Ile Ile Ala Thr Gly Ala Glu Arg Asn Ser Gly Gly Ala Ser Leu Glu
    210                 215                 220
Ser Ile Ala Thr Pro Ser Gln Pro Val Val Lys Gln Thr Arg Lys Val
225                 230                 235                 240
Gly Asn Gly Glu Tyr Leu Lys Ile Pro Thr Glu Glu Glu Leu Ser Ile
                245                 250                 255
Pro Thr Thr Met Arg Ile Gln Gln Asp
            260                 265
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<210> 139
<211> 342
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(342)
<400> 139

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gcg gtt tct caa ctc att caa gtg gga gcg tta gtc aag ttt ttg tta   48
Ala Val Ser Gln Leu Ile Gln Val Gly Ala Leu Val Lys Phe Leu Leu
  1               5                  10                  15
gcg ttt caa aaa agc act caa gct aaa atc gtt caa gtg tgt ggt ttt   96
Ala Phe Gln Lys Ser Thr Gln Ala Lys Ile Val Gln Val Cys Gly Phe
            20                  25                  30
aac ccc cat gcg ggc gaa gag ggc tta ttt ggg gaa gaa gat gaa agg   144
Asn Pro His Ala Gly Glu Glu Gly Leu Phe Gly Glu Glu Asp Glu Arg
        35                  40                  45
att tta aaa gcc att caa aag agc aac caa acg cta ggc ttt gaa tgc   192
Ile Leu Lys Ala Ile Gln Lys Ser Asn Gln Thr Leu Gly Phe Glu Cys
    50                  55                  60
ttt ttg ggg cca ctg ccg gct gat agt gct ttt gcc ccc aat aaa cga   240
Phe Leu Gly Pro Leu Pro Ala Asp Ser Ala Phe Ala Pro Asn Lys Arg
65                  70                  75                  80
aaa ata acc cct ttt tat gtg agc atg agc cat gat gtg ggg cta gcc   288
Lys Ile Thr Pro Phe Tyr Val Ser Met Ser His Asp Val Gly Leu Ala
                85                  90                  95
cct tta aaa gcg ctc tat ttt gat gaa agc att aat gtg agt ttg aac   336
Pro Leu Lys Ala Leu Tyr Phe Asp Glu Ser Ile Asn Val Ser Leu Asn
            100                 105                 110
gcc ccc                                                          342
Ala Pro
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<210> 140
<211> 114
<212> PRT
<213> Helicobacter pylori
<400> 140

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Ala Val Ser Gln Leu Ile Gln Val Gly Ala Leu Val Lys Phe Leu Leu
  1               5                  10                  15
Ala Phe Gln Lys Ser Thr Gln Ala Lys Ile Val Gln Val Cys Gly Phe
            20                  25                  30
Asn Pro His Ala Gly Glu Glu Gly Leu Phe Gly Glu Glu Asp Glu Arg
        35                  40                  45
```

```
Ile Leu Lys Ala Ile Gln Lys Ser Asn Gln Thr Leu Gly Phe Glu Cys
     50                  55                  60
Phe Leu Gly Pro Leu Pro Ala Asp Ser Ala Phe Ala Pro Asn Lys Arg
 65                  70                  75                  80
Lys Ile Thr Pro Phe Tyr Val Ser Met Ser His Asp Val Gly Leu Ala
                 85                  90                  95
Pro Leu Lys Ala Leu Tyr Phe Asp Glu Ser Ile Asn Val Ser Leu Asn
            100                 105                 110
Ala Pro
<210> 141
<211> 869
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(867)
<400> 141
ggc ggg att gcg tgc gcg aat ttg ttg cat aaa aat tca ggg atc acg   48
Gly Gly Ile Ala Cys Ala Asn Leu Leu His Lys Asn Ser Gly Ile Thr
 1               5                  10                  15
ata gat att gga ggg ggt agc acc gag tgc gcg ttg att gaa aaa ggc   96
Ile Asp Ile Gly Gly Gly Ser Thr Glu Cys Ala Leu Ile Glu Lys Gly
            20                  25                  30
aag att aag gac tta atc tcg ctt gat gtt ggg acg att cgc att aaa   144
Lys Ile Lys Asp Leu Ile Ser Leu Asp Val Gly Thr Ile Arg Ile Lys
        35                  40                  45
gaa atg ttt tta gac aaa gac tta gag gtc aaa ttg gct aaa gcc ttt   192
Glu Met Phe Leu Asp Lys Asp Leu Glu Val Lys Leu Ala Lys Ala Phe
    50                  55                  60
atc caa aaa gaa gtc tct aaa ctg ccc ttt aaa cac aaa aac gcc ttt   240
Ile Gln Lys Glu Val Ser Lys Leu Pro Phe Lys His Lys Asn Ala Phe
65                  70                  75                  80
ggg gtg ggg ggg acg atc aga gcg ttg agt aag gta ttg atg aaa cgc   288
Gly Val Gly Gly Thr Ile Arg Ala Leu Ser Lys Val Leu Met Lys Arg
                85                  90                  95
ttt tgt tac cct att gat tct ttg cat ggc tat gaa ata gat gca cat   336
Phe Cys Tyr Pro Ile Asp Ser Leu His Gly Tyr Glu Ile Asp Ala His
            100                 105                 110
aaa aat tta gcg ttc att gaa aaa atc gtc atg ctc aaa gaa gat caa   384
Lys Asn Leu Ala Phe Ile Glu Lys Ile Val Met Leu Lys Glu Asp Gln
        115                 120                 125
tta cgg ctt tta ggg gtg aat gaa gag cgt ttg gat agc atc agg agc   432
Leu Arg Leu Leu Gly Val Asn Glu Glu Arg Leu Asp Ser Ile Arg Ser
    130                 135                 140
ggg gcg ttg att tta tca gtc gtt ttg gag cat tta aaa act tct tta   480
Gly Ala Leu Ile Leu Ser Val Val Leu Glu His Leu Lys Thr Ser Leu
145                 150                 155                 160
atg atc act agt ggg gtg ggg gtg aga gaa ggc gtg ttt ttg agc gat   528
Met Ile Thr Ser Gly Val Gly Val Arg Glu Gly Val Phe Leu Ser Asp
                165                 170                 175
tta ttg cgc cat cat tac cat aaa ttc ccc ccc aat atc aac ccc tct   576
Leu Leu Arg His His Tyr His Lys Phe Pro Pro Asn Ile Asn Pro Ser
            180                 185                 190
ctc atc tct tta aaa gat cgc ttt ttg ccc cat gaa aag cac agc caa   624
Leu Ile Ser Leu Lys Asp Arg Phe Leu Pro His Glu Lys His Ser Gln
        195                 200                 205
aag gtc aaa aaa gaa tgc gtg aaa ttg ttt gaa gcc tta tcg cct ttg   672
Lys Val Lys Lys Glu Cys Val Lys Leu Phe Glu Ala Leu Ser Pro Leu
    210                 215                 220
cat aaa ata gat gaa aaa tac ctt ttc cat tta aag att gcg ggg gaa   720
His Lys Ile Asp Glu Lys Tyr Leu Phe His Leu Lys Ile Ala Gly Glu
```

```
225                 230                 235                 240
tta gcg agc atg ggt aag att tta agc gtc tat tta gcc cac aag cac   768
Leu Ala Ser Met Gly Lys Ile Leu Ser Val Tyr Leu Ala His Lys His
                245                 250                 255
agc gcg tat ttt att tta aac gct ttg agt tat ggc ttt agc cac cag   816
Ser Ala Tyr Phe Ile Leu Asn Ala Leu Ser Tyr Gly Phe Ser His Gln
            260                 265                 270
gat aga gcg atc att tgc tta tta gcc caa ttc agc cat aaa aaa atc   864
Asp Arg Ala Ile Ile Cys Leu Leu Ala Gln Phe Ser His Lys Lys Ile
        275                 280                 285
cct aa                                                            869
Pro
<210> 142
<211> 289
<212> PRT
<213> Helicobacter pylori
<400> 142
Gly Gly Ile Ala Cys Ala Asn Leu Leu His Lys Asn Ser Gly Ile Thr
  1               5                  10                  15
Ile Asp Ile Gly Gly Gly Ser Thr Glu Cys Ala Leu Ile Glu Lys Gly
             20                  25                  30
Lys Ile Lys Asp Leu Ile Ser Leu Asp Val Gly Thr Ile Arg Ile Lys
         35                  40                  45
Glu Met Phe Leu Asp Lys Asp Leu Glu Val Lys Leu Ala Lys Ala Phe
     50                  55                  60
Ile Gln Lys Glu Val Ser Lys Leu Pro Phe Lys His Lys Asn Ala Phe
 65                  70                  75                  80
Gly Val Gly Gly Thr Ile Arg Ala Leu Ser Lys Val Leu Met Lys Arg
                 85                  90                  95
Phe Cys Tyr Pro Ile Asp Ser Leu His Gly Tyr Glu Ile Asp Ala His
            100                 105                 110
Lys Asn Leu Ala Phe Ile Glu Lys Ile Val Met Leu Lys Glu Asp Gln
        115                 120                 125
Leu Arg Leu Leu Gly Val Asn Glu Glu Arg Leu Asp Ser Ile Arg Ser
    130                 135                 140
Gly Ala Leu Ile Leu Ser Val Val Leu Glu His Leu Lys Thr Ser Leu
145                 150                 155                 160
Met Ile Thr Ser Gly Val Gly Val Arg Glu Gly Val Phe Leu Ser Asp
                165                 170                 175
Leu Leu Arg His His Tyr His Lys Phe Pro Pro Asn Ile Asn Pro Ser
            180                 185                 190
Leu Ile Ser Leu Lys Asp Arg Phe Leu Pro His Glu Lys His Ser Gln
        195                 200                 205
Lys Val Lys Lys Glu Cys Val Lys Leu Phe Glu Ala Leu Ser Pro Leu
    210                 215                 220
His Lys Ile Asp Glu Lys Tyr Leu Phe His Leu Lys Ile Ala Gly Glu
225                 230                 235                 240
Leu Ala Ser Met Gly Lys Ile Leu Ser Val Tyr Leu Ala His Lys His
                245                 250                 255
Ser Ala Tyr Phe Ile Leu Asn Ala Leu Ser Tyr Gly Phe Ser His Gln
            260                 265                 270
Asp Arg Ala Ile Ile Cys Leu Leu Ala Gln Phe Ser His Lys Lys Ile
        275                 280                 285
Pro
<210> 143
<211> 609
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(609)
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<400> 143
agt ttg atc gca aac gcg ctt ttg caa tca agc ttt ttg ctc tat gcg 48
Ser Leu Ile Ala Asn Ala Leu Leu Gln Ser Ser Phe Leu Leu Tyr Ala
1 5 10 15
ttc atg cca aag agc gct gtg aaa tta gcg aat gct ttc aac aca gaa 96
Phe Met Pro Lys Ser Ala Val Lys Leu Ala Asn Ala Phe Asn Thr Glu
20 25 30
atc acg ccc gat aat tac gaa cgc ttt ttt aaa gct aaa aaa tta caa 144
Ile Thr Pro Asp Asn Tyr Glu Arg Phe Phe Lys Ala Lys Lys Leu Gln
35 40 45
gat atg att tta caa gac acc gag cct tta ttt tcc aaa atg gag aaa 192
Asp Met Ile Leu Gln Asp Thr Glu Pro Leu Phe Ser Lys Met Glu Lys
50 55 60
att gaa aag acg gaa aaa gcg gga gaa gcc tca cca gaa aaa aac gaa 240
Ile Glu Lys Thr Glu Lys Ala Gly Glu Ala Ser Pro Glu Lys Asn Glu
65 70 75 80
aaa gaa aaa aag gac gca aaa gaa aaa gcc cca cta aaa caa gaa aac 288
Lys Glu Lys Lys Asp Ala Lys Glu Lys Ala Pro Leu Lys Gln Glu Asn
85 90 95
tat atc ggc att gag gat ttc aaa aaa gta gag atc aaa gtg ggg ctt 336
Tyr Ile Gly Ile Glu Asp Phe Lys Lys Val Glu Ile Lys Val Gly Leu
100 105 110
atc aaa gaa gct caa agg att gaa aaa tcc aat aaa tta ctg cgc tta 384
Ile Lys Glu Ala Gln Arg Ile Glu Lys Ser Asn Lys Leu Leu Arg Leu
115 120 125
aaa gtg gat tta ggc gaa ggc cgt ttg agg cag att att tca ggg atc 432
Lys Val Asp Leu Gly Glu Gly Arg Leu Arg Gln Ile Ile Ser Gly Ile
130 135 140
gct ttg gat tat gag cct gaa agc ttg gtg ggt caa atg gtg tgc gtg 480
Ala Leu Asp Tyr Glu Pro Glu Ser Leu Val Gly Gln Met Val Cys Val
145 150 155 160
gtg gct aat tta aaa ccc gca aag ctt atg ggc gaa atg agt gag ggc 528
Val Ala Asn Leu Lys Pro Ala Lys Leu Met Gly Glu Met Ser Glu Gly
165 170 175
atg att tta gcg gtg cga gat agc gac aat cta gcc tta att agc ccc 576
Met Ile Leu Ala Val Arg Asp Ser Asp Asn Leu Ala Leu Ile Ser Pro
180 185 190
act aga gaa aaa att gca gga agt ttg atc agc 609
Thr Arg Glu Lys Ile Ala Gly Ser Leu Ile Ser
195 200

<210> 144
<211> 203
<212> PRT
<213> Helicobacter pylori
<400> 144
Ser Leu Ile Ala Asn Ala Leu Leu Gln Ser Ser Phe Leu Leu Tyr Ala
1 5 10 15
Phe Met Pro Lys Ser Ala Val Lys Leu Ala Asn Ala Phe Asn Thr Glu
20 25 30
Ile Thr Pro Asp Asn Tyr Glu Arg Phe Phe Lys Ala Lys Lys Leu Gln
35 40 45
Asp Met Ile Leu Gln Asp Thr Glu Pro Leu Phe Ser Lys Met Glu Lys
50 55 60
Ile Glu Lys Thr Glu Lys Ala Gly Glu Ala Ser Pro Glu Lys Asn Glu
65 70 75 80
Lys Glu Lys Lys Asp Ala Lys Glu Lys Ala Pro Leu Lys Gln Glu Asn
85 90 95
Tyr Ile Gly Ile Glu Asp Phe Lys Lys Val Glu Ile Lys Val Gly Leu
100 105 110
Ile Lys Glu Ala Gln Arg Ile Glu Lys Ser Asn Lys Leu Leu Arg Leu
115 120 125

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Lys Val Asp Leu Gly Glu Gly Arg Leu Arg Gln Ile Ile Ser Gly Ile
    130                 135                 140
Ala Leu Asp Tyr Glu Pro Glu Ser Leu Val Gly Gln Met Val Cys Val
145                 150                 155                 160
Val Ala Asn Leu Lys Pro Ala Lys Leu Met Gly Glu Met Ser Glu Gly
                165                 170                 175
Met Ile Leu Ala Val Arg Asp Ser Asp Asn Leu Ala Leu Ile Ser Pro
            180                 185                 190
Thr Arg Glu Lys Ile Ala Gly Ser Leu Ile Ser
        195                 200
<210> 145
<211> 1458
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(1458)
<400> 145
ttt gaa aac gca aaa gct gaa tgc agt tta gtt ttt att atc aat aag   48
Phe Glu Asn Ala Lys Ala Glu Cys Ser Leu Val Phe Ile Ile Asn Lys
  1               5                  10                  15
gat ttt agc cac gct tgg gtc aaa aat aaa gag ttg cta gaa acc ttt   96
Asp Phe Ser His Ala Trp Val Lys Asn Lys Glu Leu Leu Glu Thr Phe
            20                  25                  30
aaa tac gaa ggc gaa ggc gta ttt tta gac caa gaa aat aaa atc ctg   144
Lys Tyr Glu Gly Glu Gly Val Phe Leu Asp Gln Glu Asn Lys Ile Leu
        35                  40                  45
tat gcg ggc gtt aaa gaa gat gat gtg cat tta ttg aga gag agc gcg   192
Tyr Ala Gly Val Lys Glu Asp Asp Val His Leu Leu Arg Glu Ser Ala
    50                  55                  60
tgt tta gcc gtt cgc acc ctt aaa aaa ctc gct ttt aaa agc gtt aaa   240
Cys Leu Ala Val Arg Thr Leu Lys Lys Leu Ala Phe Lys Ser Val Lys
65                  70                  75                  80
gtg ggc gtt tat act tgt ggt gca cat tct aaa gat aac gcg ctt tta   288
Val Gly Val Tyr Thr Cys Gly Ala His Ser Lys Asp Asn Ala Leu Leu
                85                  90                  95
gaa aac ttg aaa gcg ctg ttt ttg ggc ttg aaa tta ggt ttg tat gaa   336
Glu Asn Leu Lys Ala Leu Phe Leu Gly Leu Lys Leu Gly Leu Tyr Glu
            100                 105                 110
tac gac act ttt aaa tcc aac aaa aaa gaa agc gtt tta aaa gaa gcc   384
Tyr Asp Thr Phe Lys Ser Asn Lys Lys Glu Ser Val Leu Lys Glu Ala
        115                 120                 125
att gtc gct tta gaa ttg cac aaa cct tgc gaa aaa act tgc gca aat   432
Ile Val Ala Leu Glu Leu His Lys Pro Cys Glu Lys Thr Cys Ala Asn
    130                 135                 140
tct tta gaa aag agt gct aaa gaa gcg tta aaa tac gct gaa atc atg   480
Ser Leu Glu Lys Ser Ala Lys Glu Ala Leu Lys Tyr Ala Glu Ile Met
145                 150                 155                 160
aca gaa agc ttg aat atc gtt aaa gat cta gtc aat acc ccc cct atg   528
Thr Glu Ser Leu Asn Ile Val Lys Asp Leu Val Asn Thr Pro Pro Met
                165                 170                 175
att ggc act ccg gtt tat atg gct gaa gtg gcg caa aaa gtg gct aaa   576
Ile Gly Thr Pro Val Tyr Met Ala Glu Val Ala Gln Lys Val Ala Lys
            180                 185                 190
gaa aac cat tta gaa atc cat gtt cat gat gaa aaa ttt tta gaa gaa   624
Glu Asn His Leu Glu Ile His Val His Asp Glu Lys Phe Leu Glu Glu
        195                 200                 205
aag aaa atg aac gcc ttt tta gcg gtc aat aaa gcc tct ctt agc gtc   672
Lys Lys Met Asn Ala Phe Leu Ala Val Asn Lys Ala Ser Leu Ser Val
    210                 215                 220
aat cct cct cgc ttg atc cat tta gtc tat aag cct aaa aaa gcg aag   720
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Asn Pro Pro Arg Leu Ile His Leu Val Tyr Lys Pro Lys Lys Ala Lys
225                 230                 235                 240
aaa aaa atc gct tta gtg ggt aag ggc ttg act tat gat tgt ggg ggt   768
Lys Lys Ile Ala Leu Val Gly Lys Gly Leu Thr Tyr Asp Cys Gly Gly
                245                 250                 255
ttg agc ttg aaa ccg gcc gat tac atg gtt act atg aaa gcg gat aaa   816
Leu Ser Leu Lys Pro Ala Asp Tyr Met Val Thr Met Lys Ala Asp Lys
            260                 265                 270
ggc ggt ggc tct gcg gtg att ggg ctt tta aac gca tta gcc aaa cta   864
Gly Gly Gly Ser Ala Val Ile Gly Leu Leu Asn Ala Leu Ala Lys Leu
        275                 280                 285
ggc gtg gag gct gaa gtg cat ggc att att ggg gct aca gaa aac atg   912
Gly Val Glu Ala Glu Val His Gly Ile Ile Gly Ala Thr Glu Asn Met
    290                 295                 300
ata ggc cca gcc gct tat aaa cca gat gat att ttg atc tcc aaa gaa   960
Ile Gly Pro Ala Ala Tyr Lys Pro Asp Asp Ile Leu Ile Ser Lys Glu
305                 310                 315                 320
ggc aag agc ata gag gtc cgt aat acc gac gct gag ggg cgt ttg gtt  1008
Gly Lys Ser Ile Glu Val Arg Asn Thr Asp Ala Glu Gly Arg Leu Val
                325                 330                 335
tta gcg gat tgt ttg agc tac gct caa gat tta aac cct gat gtg atc  1056
Leu Ala Asp Cys Leu Ser Tyr Ala Gln Asp Leu Asn Pro Asp Val Ile
            340                 345                 350
gtg gat ttt gcg acc ctt act ggg gca tgc gtt gta ggc tta ggc gaa  1104
Val Asp Phe Ala Thr Leu Thr Gly Ala Cys Val Val Gly Leu Gly Glu
        355                 360                 365
ttc act tca gcg atc atg ggg cat aat gaa gag tta aaa aac ctc ttt  1152
Phe Thr Ser Ala Ile Met Gly His Asn Glu Glu Leu Lys Asn Leu Phe
    370                 375                 380
gaa act tca ggg tta gaa tcc ggc gaa tta tta gcc aaa ctc ccc ttt  1200
Glu Thr Ser Gly Leu Glu Ser Gly Glu Leu Leu Ala Lys Leu Pro Phe
385                 390                 395                 400
aac cgc cat tta aag aaa ttg att gaa tct aaa atc gct gat gtg tgc  1248
Asn Arg His Leu Lys Lys Leu Ile Glu Ser Lys Ile Ala Asp Val Cys
                405                 410                 415
aat att tct tct tca cgc tat ggc ggt gcg atc aca gcg ggc ttg ttt  1296
Asn Ile Ser Ser Ser Arg Tyr Gly Gly Ala Ile Thr Ala Gly Leu Phe
            420                 425                 430
tta aat gaa ttt att aga gat gag ttt aag gat aag tgg cta cac att  1344
Leu Asn Glu Phe Ile Arg Asp Glu Phe Lys Asp Lys Trp Leu His Ile
        435                 440                 445
gac att gca ggc cct gct tat gtg gaa aaa gaa tgg gat gtg aat agc  1392
Asp Ile Ala Gly Pro Ala Tyr Val Glu Lys Glu Trp Asp Val Asn Ser
    450                 455                 460
ttt gga gcg agt ggg gct ggc gtg aga gct tgc aca gct ttt gtg gaa  1440
Phe Gly Ala Ser Gly Ala Gly Val Arg Ala Cys Thr Ala Phe Val Glu
465                 470                 475                 480
gag ctt ttg aaa aag gct                                         1458
Glu Leu Leu Lys Lys Ala
                485
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<210> 146
<211> 486
<212> PRT
<213> Helicobacter pylori
<400> 146

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Phe Glu Asn Ala Lys Ala Glu Cys Ser Leu Val Phe Ile Ile Asn Lys
  1               5                  10                  15
Asp Phe Ser His Ala Trp Val Lys Asn Lys Glu Leu Leu Glu Thr Phe
            20                  25                  30
Lys Tyr Glu Gly Glu Gly Val Phe Leu Asp Gln Glu Asn Lys Ile Leu
        35                  40                  45
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Tyr Ala Gly Val Lys Glu Asp Asp Val His Leu Leu Arg Glu Ser Ala
     50                  55                  60
Cys Leu Ala Val Arg Thr Leu Lys Lys Leu Ala Phe Lys Ser Val Lys
 65                  70                  75                  80
Val Gly Val Tyr Thr Cys Gly Ala His Ser Lys Asp Asn Ala Leu Leu
                 85                  90                  95
Glu Asn Leu Lys Ala Leu Phe Leu Gly Leu Lys Leu Gly Leu Tyr Glu
            100                 105                 110
Tyr Asp Thr Phe Lys Ser Asn Lys Lys Glu Ser Val Leu Lys Glu Ala
        115                 120                 125
Ile Val Ala Leu Glu Leu His Lys Pro Cys Glu Lys Thr Cys Ala Asn
    130                 135                 140
Ser Leu Glu Lys Ser Ala Lys Glu Ala Leu Lys Tyr Ala Glu Ile Met
145                 150                 155                 160
Thr Glu Ser Leu Asn Ile Val Lys Asp Leu Val Asn Thr Pro Pro Met
                165                 170                 175
Ile Gly Thr Pro Val Tyr Met Ala Glu Val Ala Gln Lys Val Ala Lys
            180                 185                 190
Glu Asn His Leu Glu Ile His Val His Asp Glu Lys Phe Leu Glu Glu
        195                 200                 205
Lys Lys Met Asn Ala Phe Leu Ala Val Asn Lys Ala Ser Leu Ser Val
    210                 215                 220
Asn Pro Pro Arg Leu Ile His Leu Val Tyr Lys Pro Lys Lys Ala Lys
225                 230                 235                 240
Lys Lys Ile Ala Leu Val Gly Lys Gly Leu Thr Tyr Asp Cys Gly Gly
                245                 250                 255
Leu Ser Leu Lys Pro Ala Asp Tyr Met Val Thr Met Lys Ala Asp Lys
            260                 265                 270
Gly Gly Gly Ser Ala Val Ile Gly Leu Leu Asn Ala Leu Ala Lys Leu
        275                 280                 285
Gly Val Glu Ala Glu Val His Gly Ile Ile Gly Ala Thr Glu Asn Met
    290                 295                 300
Ile Gly Pro Ala Ala Tyr Lys Pro Asp Asp Ile Leu Ile Ser Lys Glu
305                 310                 315                 320
Gly Lys Ser Ile Glu Val Arg Asn Thr Asp Ala Glu Gly Arg Leu Val
                325                 330                 335
Leu Ala Asp Cys Leu Ser Tyr Ala Gln Asp Leu Asn Pro Asp Val Ile
            340                 345                 350
Val Asp Phe Ala Thr Leu Thr Gly Ala Cys Val Val Gly Leu Gly Glu
        355                 360                 365
Phe Thr Ser Ala Ile Met Gly His Asn Glu Glu Leu Lys Asn Leu Phe
    370                 375                 380
Glu Thr Ser Gly Leu Glu Ser Gly Glu Leu Leu Ala Lys Leu Pro Phe
385                 390                 395                 400
Asn Arg His Leu Lys Lys Leu Ile Glu Ser Lys Ile Ala Asp Val Cys
                405                 410                 415
Asn Ile Ser Ser Ser Arg Tyr Gly Gly Ala Ile Thr Ala Gly Leu Phe
            420                 425                 430
Leu Asn Glu Phe Ile Arg Asp Glu Phe Lys Asp Lys Trp Leu His Ile
        435                 440                 445
Asp Ile Ala Gly Pro Ala Tyr Val Glu Lys Glu Trp Asp Val Asn Ser
    450                 455                 460
Phe Gly Ala Ser Gly Ala Gly Val Arg Ala Cys Thr Ala Phe Val Glu
465                 470                 475                 480
Glu Leu Leu Lys Lys Ala
                485
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<210> 147
<211> 960
<212> DNA
<213> Helicobacter pylori
<220>

<221> CDS
<222> (1)..(960)
<400> 147

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gat gtt att aaa aaa gtt acg acc cca aag ggt ggc att gaa atc tta   48
Asp Val Ile Lys Lys Val Thr Thr Pro Lys Gly Gly Ile Glu Ile Leu
 1               5                  10                  15
agg act tta att gat ttt acg ccc aaa att gaa aac gcc ctg aat tta   96
Arg Thr Leu Ile Asp Phe Thr Pro Lys Ile Glu Asn Ala Leu Asn Leu
            20                  25                  30
gcg gcc aaa agc cat aag ggg caa tac aga aaa agc ggc gag cct tat  144
Ala Ala Lys Ser His Lys Gly Gln Tyr Arg Lys Ser Gly Glu Pro Tyr
        35                  40                  45
att gtc cat cct att tgc gtg gca agc ttg gta gcg ttt tgt ggg ggc  192
Ile Val His Pro Ile Cys Val Ala Ser Leu Val Ala Phe Cys Gly Gly
    50                  55                  60
gat gag gcg atg gtg tgt gct gcg ctt ttg cat gat gtg gtg gaa gac  240
Asp Glu Ala Met Val Cys Ala Ala Leu Leu His Asp Val Val Glu Asp
65                  70                  75                  80
acg cct tgt aag att gaa acg att gag caa gaa ttt ggg caa gat gtg  288
Thr Pro Cys Lys Ile Glu Thr Ile Glu Gln Glu Phe Gly Gln Asp Val
                85                  90                  95
gct aat tta gtg gat gcg ctc act aaa atc act gaa atc agg aaa gaa  336
Ala Asn Leu Val Asp Ala Leu Thr Lys Ile Thr Glu Ile Arg Lys Glu
            100                 105                 110
gaa tta ggc gtg agc tct caa gat ccc aga atg gtg gtt tca gcg ctc  384
Glu Leu Gly Val Ser Ser Gln Asp Pro Arg Met Val Val Ser Ala Leu
        115                 120                 125
act ttc aga aag att tta att agc gcg ata caa gat cca aga gcc tta  432
Thr Phe Arg Lys Ile Leu Ile Ser Ala Ile Gln Asp Pro Arg Ala Leu
    130                 135                 140
gtg gta aag att agc gac agg ttg cac aac atg ctc acc tta gac gcc  480
Val Val Lys Ile Ser Asp Arg Leu His Asn Met Leu Thr Leu Asp Ala
145                 150                 155                 160
ttg cct cat gac aag caa gtg cgt att tct aaa gag act cta gcg gtg  528
Leu Pro His Asp Lys Gln Val Arg Ile Ser Lys Glu Thr Leu Ala Val
                165                 170                 175
tat gcc cct ata gcg agc cga ttg ggc atg tct tca atc aaa aat gaa  576
Tyr Ala Pro Ile Ala Ser Arg Leu Gly Met Ser Ser Ile Lys Asn Glu
            180                 185                 190
tta gaa gac aag agc ttt tat tat att tat cca gaa gag tat aaa aat  624
Leu Glu Asp Lys Ser Phe Tyr Tyr Ile Tyr Pro Glu Glu Tyr Lys Asn
        195                 200                 205
atc aag gaa tat ttg cac aaa aac aag cag tct tta ctc tta aag ctc  672
Ile Lys Glu Tyr Leu His Lys Asn Lys Gln Ser Leu Leu Leu Lys Leu
    210                 215                 220
aac gct ttt gcg agc aag tta gaa aaa aaa ctt ttt gat agt ggg ttt  720
Asn Ala Phe Ala Ser Lys Leu Glu Lys Lys Leu Phe Asp Ser Gly Phe
225                 230                 235                 240
agc cat tcg gat ttt aaa ctc gtt aca agg gtg aaa cgc cct tat tct  768
Ser His Ser Asp Phe Lys Leu Val Thr Arg Val Lys Arg Pro Tyr Ser
                245                 250                 255
atc tat ctt aag atg caa cga aag ggc gcg gtt aat att gat gaa att  816
Ile Tyr Leu Lys Met Gln Arg Lys Gly Ala Val Asn Ile Asp Glu Ile
            260                 265                 270
ttg gac ttg tta gcc att agg att tta ttg aaa aac ccg att gat tgc  864
Leu Asp Leu Leu Ala Ile Arg Ile Leu Leu Lys Asn Pro Ile Asp Cys
        275                 280                 285
tat aaa gtt tta ggg att atc cat ttg aat ttc aaa ccc att gtc tct  912
Tyr Lys Val Leu Gly Ile Ile His Leu Asn Phe Lys Pro Ile Val Ser
    290                 295                 300
cgt ttt aaa gat tac atc gct ttg ccc aaa gaa aat ggc tat aag acg  960
```

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Arg Phe Lys Asp Tyr Ile Ala Leu Pro Lys Glu Asn Gly Tyr Lys Thr
305                 310                 315                 320
<210> 148
<211> 320
<212> PRT
<213> Helicobacter pylori
<400> 148
Asp Val Ile Lys Lys Val Thr Thr Pro Lys Gly Gly Ile Glu Ile Leu
 1               5                  10                  15
Arg Thr Leu Ile Asp Phe Thr Pro Lys Ile Glu Asn Ala Leu Asn Leu
            20                  25                  30
Ala Ala Lys Ser His Lys Gly Gln Tyr Arg Lys Ser Gly Glu Pro Tyr
        35                  40                  45
Ile Val His Pro Ile Cys Val Ala Ser Leu Val Ala Phe Cys Gly Gly
    50                  55                  60
Asp Glu Ala Met Val Cys Ala Ala Leu Leu His Asp Val Val Glu Asp
65                  70                  75                  80
Thr Pro Cys Lys Ile Glu Thr Ile Glu Gln Glu Phe Gly Gln Asp Val
                85                  90                  95
Ala Asn Leu Val Asp Ala Leu Thr Lys Ile Thr Glu Ile Arg Lys Glu
            100                 105                 110
Glu Leu Gly Val Ser Ser Gln Asp Pro Arg Met Val Val Ser Ala Leu
        115                 120                 125
Thr Phe Arg Lys Ile Leu Ile Ser Ala Ile Gln Asp Pro Arg Ala Leu
    130                 135                 140
Val Val Lys Ile Ser Asp Arg Leu His Asn Met Leu Thr Leu Asp Ala
145                 150                 155                 160
Leu Pro His Asp Lys Gln Val Arg Ile Ser Lys Glu Thr Leu Ala Val
                165                 170                 175
Tyr Ala Pro Ile Ala Ser Arg Leu Gly Met Ser Ser Ile Lys Asn Glu
            180                 185                 190
Leu Glu Asp Lys Ser Phe Tyr Tyr Ile Tyr Pro Glu Glu Tyr Lys Asn
        195                 200                 205
Ile Lys Glu Tyr Leu His Lys Asn Lys Gln Ser Leu Leu Leu Lys Leu
    210                 215                 220
Asn Ala Phe Ala Ser Lys Leu Glu Lys Lys Leu Phe Asp Ser Gly Phe
225                 230                 235                 240
Ser His Ser Asp Phe Lys Leu Val Thr Arg Val Lys Arg Pro Tyr Ser
                245                 250                 255
Ile Tyr Leu Lys Met Gln Arg Lys Gly Ala Val Asn Ile Asp Glu Ile
            260                 265                 270
Leu Asp Leu Leu Ala Ile Arg Ile Leu Leu Lys Asn Pro Ile Asp Cys
        275                 280                 285
Tyr Lys Val Leu Gly Ile Ile His Leu Asn Phe Lys Pro Ile Val Ser
    290                 295                 300
Arg Phe Lys Asp Tyr Ile Ala Leu Pro Lys Glu Asn Gly Tyr Lys Thr
305                 310                 315                 320
<210> 149
<211> 324
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(324)
<400> 149
ttg cta gcg att gtg ttg agc att tct act ttt att gca caa ggt aag   48
Leu Leu Ala Ile Val Leu Ser Ile Ser Thr Phe Ile Ala Gln Gly Lys
 1               5                  10                  15
att aag gtc agt ctc cct aac gct aaa aat gcg gaa aaa tcc cag cca   96
Ile Lys Val Ser Leu Pro Asn Ala Lys Asn Ala Glu Lys Ser Gln Pro
            20                  25                  30
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```
aac gat caa aaa gtg gtg gtc atc tct gta gat gag cat gac aat att   144
Asn Asp Gln Lys Val Val Val Ile Ser Val Asp Glu His Asp Asn Ile
         35                  40                  45
ttc gta gat gac aaa ccg atg aat tta gaa gct ttg agc gct gta gtc   192
Phe Val Asp Asp Lys Pro Met Asn Leu Glu Ala Leu Ser Ala Val Val
     50                  55                  60
aaa caa aca gac cct aaa acc ctt ata gac tta aaa agc gac aaa agc   240
Lys Gln Thr Asp Pro Lys Thr Leu Ile Asp Leu Lys Ser Asp Lys Ser
 65                  70                  75                  80
tct cgt ttt gaa act ttt atc agc att atg gat att tta aaa gag cat   288
Ser Arg Phe Glu Thr Phe Ile Ser Ile Met Asp Ile Leu Lys Glu His
                 85                  90                  95
aat cat gaa aat ttc tcc atc tcc acg caa gct cag                  324
Asn His Glu Asn Phe Ser Ile Ser Thr Gln Ala Gln
            100                 105
<210> 150
<211> 108
<212> PRT
<213> Helicobacter pylori
<400> 150
Leu Leu Ala Ile Val Leu Ser Ile Ser Thr Phe Ile Ala Gln Gly Lys
  1               5                  10                  15
Ile Lys Val Ser Leu Pro Asn Ala Lys Asn Ala Glu Lys Ser Gln Pro
             20                  25                  30
Asn Asp Gln Lys Val Val Val Ile Ser Val Asp Glu His Asp Asn Ile
         35                  40                  45
Phe Val Asp Asp Lys Pro Met Asn Leu Glu Ala Leu Ser Ala Val Val
     50                  55                  60
Lys Gln Thr Asp Pro Lys Thr Leu Ile Asp Leu Lys Ser Asp Lys Ser
 65                  70                  75                  80
Ser Arg Phe Glu Thr Phe Ile Ser Ile Met Asp Ile Leu Lys Glu His
                 85                  90                  95
Asn His Glu Asn Phe Ser Ile Ser Thr Gln Ala Gln
            100                 105
<210> 151
<211> 837
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(837)
<400> 151
gac agc aaa aaa gac gct tgc ggg ttc atc tat gag atc agc gag ttc   48
Asp Ser Lys Lys Asp Ala Cys Gly Phe Ile Tyr Glu Ile Ser Glu Phe
  1               5                  10                  15
atg aaa gcc tat acc gca ttg cta aaa aaa caa gac cga tac gtc tat   96
Met Lys Ala Tyr Thr Ala Leu Leu Lys Lys Gln Asp Arg Tyr Val Tyr
             20                  25                  30
tta ttg agg tat ctc ccc tct agg tat tgg gcc agc att tta acg act   144
Leu Leu Arg Tyr Leu Pro Ser Arg Tyr Trp Ala Ser Ile Leu Thr Thr
         35                  40                  45
gcc ctt tat gtc aaa tac cct gat ttt gac gct ttg aaa aag ctt ttg   192
Ala Leu Tyr Val Lys Tyr Pro Asp Phe Asp Ala Leu Lys Lys Leu Leu
     50                  55                  60
gtg tct tat tat tac caa act tgg att gca gga ggc acg atc acg cgc   240
Val Ser Tyr Tyr Tyr Gln Thr Trp Ile Ala Gly Gly Thr Ile Thr Arg
 65                  70                  75                  80
atc aag caa acc agt atc aac att atc aaa aac gtt aaa agc aat aag   288
Ile Lys Gln Thr Ser Ile Asn Ile Ile Lys Asn Val Lys Ser Asn Lys
                 85                  90                  95
agc gtt gaa acc atc aaa gag ctt ata ttg aat agc atc gac tct tat   336
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```
Ser Val Glu Thr Ile Lys Glu Leu Ile Leu Asn Ser Ile Asp Ser Tyr
          100                 105                 110
aac acc ttt gat caa tac ctc tat aac tta tgg gat agc tct tct gtt   384
Asn Thr Phe Asp Gln Tyr Leu Tyr Asn Leu Trp Asp Ser Ser Ser Val
      115                 120                 125
tat cat agc aaa tgg gtg cgt cct gtc tta gcc cta gct aat tat ttc   432
Tyr His Ser Lys Trp Val Arg Pro Val Leu Ala Leu Ala Asn Tyr Phe
  130                 135                 140
atg gca gat gaa gag aaa ccc cat ttt atc gct atg gat gcc gaa acc   480
Met Ala Asp Glu Glu Lys Pro His Phe Ile Ala Met Asp Ala Glu Thr
145                 150                 155                 160
caa gtg gag cat att ttg cca caa acg ccc aaa aga ggc agt caa tgg   528
Gln Val Glu His Ile Leu Pro Gln Thr Pro Lys Arg Gly Ser Gln Trp
              165                 170                 175
aac gcg gat ttt gac aaa gaa aaa aga gaa gaa tgg gta aat aat atc   576
Asn Ala Asp Phe Asp Lys Glu Lys Arg Glu Glu Trp Val Asn Asn Ile
          180                 185                 190
gcg aat tta acc ctt tta aag cgt aaa aag aac gcg cat gct tta aac   624
Ala Asn Leu Thr Leu Leu Lys Arg Lys Lys Asn Ala His Ala Leu Asn
      195                 200                 205
ggg gat ttt gat gaa aaa aga aaa att tat gga ggc aaa gac acg agc   672
Gly Asp Phe Asp Glu Lys Arg Lys Ile Tyr Gly Gly Lys Asp Thr Ser
  210                 215                 220
aaa gtg att agc tgt tat gac atc act aaa gaa ttg tat agc aat tat   720
Lys Val Ile Ser Cys Tyr Asp Ile Thr Lys Glu Leu Tyr Ser Asn Tyr
225                 230                 235                 240
agg aag tgg aat gag aag tcc ctc caa gag cga tac aaa tct ttg tat   768
Arg Lys Trp Asn Glu Lys Ser Leu Gln Glu Arg Tyr Lys Ser Leu Tyr
              245                 250                 255
aac act atc acg cct gtt tta cac ata gag ggg caa gaa gat gat ttt   816
Asn Thr Ile Thr Pro Val Leu His Ile Glu Gly Gln Glu Asp Asp Phe
          260                 265                 270
gaa gat gat ttt gat cta gaa                                      837
Glu Asp Asp Phe Asp Leu Glu
      275
<210> 152
<211> 279
<212> PRT
<213> Helicobacter pylori
<400> 152
Asp Ser Lys Lys Asp Ala Cys Gly Phe Ile Tyr Glu Ile Ser Glu Phe
  1               5                  10                  15
Met Lys Ala Tyr Thr Ala Leu Leu Lys Lys Gln Asp Arg Tyr Val Tyr
             20                  25                  30
Leu Leu Arg Tyr Leu Pro Ser Arg Tyr Trp Ala Ser Ile Leu Thr Thr
         35                  40                  45
Ala Leu Tyr Val Lys Tyr Pro Asp Phe Asp Ala Leu Lys Lys Leu Leu
     50                  55                  60
Val Ser Tyr Tyr Tyr Gln Thr Trp Ile Ala Gly Gly Thr Ile Thr Arg
 65                  70                  75                  80
Ile Lys Gln Thr Ser Ile Asn Ile Ile Lys Asn Val Lys Ser Asn Lys
                 85                  90                  95
Ser Val Glu Thr Ile Lys Glu Leu Ile Leu Asn Ser Ile Asp Ser Tyr
            100                 105                 110
Asn Thr Phe Asp Gln Tyr Leu Tyr Asn Leu Trp Asp Ser Ser Ser Val
        115                 120                 125
Tyr His Ser Lys Trp Val Arg Pro Val Leu Ala Leu Ala Asn Tyr Phe
    130                 135                 140
Met Ala Asp Glu Glu Lys Pro His Phe Ile Ala Met Asp Ala Glu Thr
145                 150                 155                 160
Gln Val Glu His Ile Leu Pro Gln Thr Pro Lys Arg Gly Ser Gln Trp
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                165                 170                 175
Asn Ala Asp Phe Asp Lys Glu Lys Arg Glu Glu Trp Val Asn Asn Ile
            180                 185                 190
Ala Asn Leu Thr Leu Leu Lys Arg Lys Lys Asn Ala His Ala Leu Asn
        195                 200                 205
Gly Asp Phe Asp Glu Lys Arg Lys Ile Tyr Gly Gly Lys Asp Thr Ser
    210                 215                 220
Lys Val Ile Ser Cys Tyr Asp Ile Thr Lys Glu Leu Tyr Ser Asn Tyr
225                 230                 235                 240
Arg Lys Trp Asn Glu Lys Ser Leu Gln Glu Arg Tyr Lys Ser Leu Tyr
                245                 250                 255
Asn Thr Ile Thr Pro Val Leu His Ile Glu Gly Gln Glu Asp Asp Phe
            260                 265                 270
Glu Asp Asp Phe Asp Leu Glu
        275
<210> 153
<211> 684
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(684)
<400> 153
ttg atg ctc cac tat gct gga gaa ttg gct aaa aaa cgc aaa gaa aaa   48
Leu Met Leu His Tyr Ala Gly Glu Leu Ala Lys Lys Arg Lys Glu Lys
  1               5                  10                  15
ggc att aag ctt aac tat gta gaa gcg gta gct ttg att agt gcc cat   96
Gly Ile Lys Leu Asn Tyr Val Glu Ala Val Ala Leu Ile Ser Ala His
             20                  25                  30
att atg gaa gaa gcg aga gct ggt aaa aag act gcg gct gaa ttg atg   144
Ile Met Glu Glu Ala Arg Ala Gly Lys Lys Thr Ala Ala Glu Leu Met
         35                  40                  45
caa gaa ggg cgc act ctt tta aaa ccg gat gat gtg atg gat ggc gtg   192
Gln Glu Gly Arg Thr Leu Leu Lys Pro Asp Asp Val Met Asp Gly Val
     50                  55                  60
gca agc atg atc cat gaa gtg ggt att gaa gcg atg ttt cct gat ggg   240
Ala Ser Met Ile His Glu Val Gly Ile Glu Ala Met Phe Pro Asp Gly
 65                  70                  75                  80
aca aaa ctc gta acc gtg cat acc cct att gag gcc aat ggt aaa tta   288
Thr Lys Leu Val Thr Val His Thr Pro Ile Glu Ala Asn Gly Lys Leu
                 85                  90                  95
gtt cct ggt gag ttg ttc tta aaa aat gaa gac atc act atc aac gaa   336
Val Pro Gly Glu Leu Phe Leu Lys Asn Glu Asp Ile Thr Ile Asn Glu
            100                 105                 110
ggc aaa aaa gcc gtt agc gtg aaa gtt aaa aat gtt ggc gac aga ccg   384
Gly Lys Lys Ala Val Ser Val Lys Val Lys Asn Val Gly Asp Arg Pro
        115                 120                 125
gtt caa atc ggc tca cac ttc cat ttc ttt gaa gtg aat aga tgc tta   432
Val Gln Ile Gly Ser His Phe His Phe Phe Glu Val Asn Arg Cys Leu
    130                 135                 140
gac ttt gac aga gaa aaa act ttc ggt aaa cgc tta gac att gcg agc   480
Asp Phe Asp Arg Glu Lys Thr Phe Gly Lys Arg Leu Asp Ile Ala Ser
145                 150                 155                 160
ggg aca gcg gta agg ttt gag cct ggc gaa gaa aaa tcc gta gaa ttg   528
Gly Thr Ala Val Arg Phe Glu Pro Gly Glu Glu Lys Ser Val Glu Leu
                165                 170                 175
att gac att ggc ggt aac aga aga atc ttt gga ttt aac gcg ttg gtt   576
Ile Asp Ile Gly Gly Asn Arg Arg Ile Phe Gly Phe Asn Ala Leu Val
            180                 185                 190
gat agg caa gca gac aac gaa agc aaa aaa att gct tta cac aga gct   624
Asp Arg Gln Ala Asp Asn Glu Ser Lys Lys Ile Ala Leu His Arg Ala
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       195                 200                 205
aaa gag cgt ggt ttt cat ggc gct aaa agc gat gac aac tat gta aaa   672
Lys Glu Arg Gly Phe His Gly Ala Lys Ser Asp Asp Asn Tyr Val Lys
    210                 215                 220
aca att aag gag                                                684
Thr Ile Lys Glu
225
<210> 154
<211> 228
<212> PRT
<213> Helicobacter pylori
<400> 154
Leu Met Leu His Tyr Ala Gly Glu Leu Ala Lys Lys Arg Lys Glu Lys
  1               5                  10                  15
Gly Ile Lys Leu Asn Tyr Val Glu Ala Val Ala Leu Ile Ser Ala His
             20                  25                  30
Ile Met Glu Glu Ala Arg Ala Gly Lys Lys Thr Ala Ala Glu Leu Met
         35                  40                  45
Gln Glu Gly Arg Thr Leu Leu Lys Pro Asp Asp Val Met Asp Gly Val
     50                  55                  60
Ala Ser Met Ile His Glu Val Gly Ile Glu Ala Met Phe Pro Asp Gly
 65                  70                  75                  80
Thr Lys Leu Val Thr Val His Thr Pro Ile Glu Ala Asn Gly Lys Leu
                 85                  90                  95
Val Pro Gly Glu Leu Phe Leu Lys Asn Glu Asp Ile Thr Ile Asn Glu
            100                 105                 110
Gly Lys Lys Ala Val Ser Val Lys Val Lys Asn Val Gly Asp Arg Pro
        115                 120                 125
Val Gln Ile Gly Ser His Phe His Phe Phe Glu Val Asn Arg Cys Leu
    130                 135                 140
Asp Phe Asp Arg Glu Lys Thr Phe Gly Lys Arg Leu Asp Ile Ala Ser
145                 150                 155                 160
Gly Thr Ala Val Arg Phe Glu Pro Gly Glu Glu Lys Ser Val Glu Leu
                165                 170                 175
Ile Asp Ile Gly Gly Asn Arg Arg Ile Phe Gly Phe Asn Ala Leu Val
            180                 185                 190
Asp Arg Gln Ala Asp Asn Glu Ser Lys Lys Ile Ala Leu His Arg Ala
        195                 200                 205
Lys Glu Arg Gly Phe His Gly Ala Lys Ser Asp Asp Asn Tyr Val Lys
    210                 215                 220
Thr Ile Lys Glu
225
<210> 155
<211> 486
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(486)
<400> 155
tta gaa gag caa aag gat aaa tct tac aag gtt gtt gaa gaa tac ccc    48
Leu Glu Glu Gln Lys Asp Lys Ser Tyr Lys Val Val Glu Glu Tyr Pro
  1               5                  10                  15
agc tca aga acc cac att ata gtg cgc gat ttg caa ggc aat gaa cgc    96
Ser Ser Arg Thr His Ile Ile Val Arg Asp Leu Gln Gly Asn Glu Arg
             20                  25                  30
gtg tta agc aat gaa gag att caa aag ctc atc aaa gaa gaa gaa gct   144
Val Leu Ser Asn Glu Glu Ile Gln Lys Leu Ile Lys Glu Glu Glu Ala
         35                  40                  45
aaa att gat aac ggc acg agc aag ctt gtc cag cct aat aat gga ggg   192
Lys Ile Asp Asn Gly Thr Ser Lys Leu Val Gln Pro Asn Asn Gly Gly
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     50                  55                  60
agt aat gaa ggc tca ggc ttt ggc ttg ggg agc gcg att tta ggg agc   240
Ser Asn Glu Gly Ser Gly Phe Gly Leu Gly Ser Ala Ile Leu Gly Ser
 65                  70                  75                  80
gcg gcg ggg gcg att tta ggg agt tat att ggt aat aag ctt ttc aat   288
Ala Ala Gly Ala Ile Leu Gly Ser Tyr Ile Gly Asn Lys Leu Phe Asn
                 85                  90                  95
aac cct aat tac cag caa aac gcc caa cgg acc tac aaa tcc cca caa   336
Asn Pro Asn Tyr Gln Gln Asn Ala Gln Arg Thr Tyr Lys Ser Pro Gln
            100                 105                 110
gct tac caa cgc tct caa aat tcc ttt tct aaa agt gcg ccc agt gct   384
Ala Tyr Gln Arg Ser Gln Asn Ser Phe Ser Lys Ser Ala Pro Ser Ala
        115                 120                 125
tca agc atg ggc gga gcg agt aag gga cag agc ggg ttt ttt ggc tct   432
Ser Ser Met Gly Gly Ala Ser Lys Gly Gln Ser Gly Phe Phe Gly Ser
    130                 135                 140
agt agg cct act agt tca ccg gcg gta agc tct ggg aca agg ggc ttt   480
Ser Arg Pro Thr Ser Ser Pro Ala Val Ser Ser Gly Thr Arg Gly Phe
145                 150                 155                 160
aac tca                                                          486
Asn Ser
<210> 156
<211> 162
<212> PRT
<213> Helicobacter pylori
<400> 156
Leu Glu Glu Gln Lys Asp Lys Ser Tyr Lys Val Val Glu Glu Tyr Pro
  1               5                  10                  15
Ser Ser Arg Thr His Ile Ile Val Arg Asp Leu Gln Gly Asn Glu Arg
             20                  25                  30
Val Leu Ser Asn Glu Glu Ile Gln Lys Leu Ile Lys Glu Glu Glu Ala
         35                  40                  45
Lys Ile Asp Asn Gly Thr Ser Lys Leu Val Gln Pro Asn Asn Gly Gly
     50                  55                  60
Ser Asn Glu Gly Ser Gly Phe Gly Leu Gly Ser Ala Ile Leu Gly Ser
 65                  70                  75                  80
Ala Ala Gly Ala Ile Leu Gly Ser Tyr Ile Gly Asn Lys Leu Phe Asn
                 85                  90                  95
Asn Pro Asn Tyr Gln Gln Asn Ala Gln Arg Thr Tyr Lys Ser Pro Gln
            100                 105                 110
Ala Tyr Gln Arg Ser Gln Asn Ser Phe Ser Lys Ser Ala Pro Ser Ala
        115                 120                 125
Ser Ser Met Gly Gly Ala Ser Lys Gly Gln Ser Gly Phe Phe Gly Ser
    130                 135                 140
Ser Arg Pro Thr Ser Ser Pro Ala Val Ser Ser Gly Thr Arg Gly Phe
145                 150                 155                 160
Asn Ser
<210> 157
<211> 1032
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(1032)
<400> 157
act ttt ttg caa gtt agg gtt caa ggg gaa gtg agt aat ttg act atc    48
Thr Phe Leu Gln Val Arg Val Gln Gly Glu Val Ser Asn Leu Thr Ile
  1               5                  10                  15
cat aag gtg agc ggc cat gcg tat ttt tcg ctc aaa gac agc cag tcg    96
His Lys Val Ser Gly His Ala Tyr Phe Ser Leu Lys Asp Ser Gln Ser
             20                  25                  30
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gtt att aaa tgc gtg ctg ttt aaa ggg aac gct aac agg ctc aaa ttc   144
Val Ile Lys Cys Val Leu Phe Lys Gly Asn Ala Asn Arg Leu Lys Phe
        35                  40                  45
gct tta aaa gaa ggg cag gaa gtg gtt gtt ttt ggg ggt att agc gtg   192
Ala Leu Lys Glu Gly Gln Glu Val Val Val Phe Gly Gly Ile Ser Val
    50                  55                  60
tat gtc cca agg ggg gat tat caa atc aat tgc ttt gaa ata gag cct   240
Tyr Val Pro Arg Gly Asp Tyr Gln Ile Asn Cys Phe Glu Ile Glu Pro
65                  70                  75                  80
aag gat ata ggt tca tta act tta gct tta gag caa ttg aaa gaa aaa   288
Lys Asp Ile Gly Ser Leu Thr Leu Ala Leu Glu Gln Leu Lys Glu Lys
                85                  90                  95
tta cgc ctt aaa ggc tat ttt gat gaa gaa aat aaa tta ccc aaa ccg   336
Leu Arg Leu Lys Gly Tyr Phe Asp Glu Glu Asn Lys Leu Pro Lys Pro
            100                 105                 110
cat ttt cct aaa cga gtg gca gtc atc act tct caa aat tca gcc gct   384
His Phe Pro Lys Arg Val Ala Val Ile Thr Ser Gln Asn Ser Ala Ala
        115                 120                 125
tgg gcg gac atg aaa aag atc gct tcc aaa cga tgg ccg atg tgt gaa   432
Trp Ala Asp Met Lys Lys Ile Ala Ser Lys Arg Trp Pro Met Cys Glu
    130                 135                 140
tta gtt tgt atc aac acc tta atg caa ggg gag ggc tgc gtt caa agc   480
Leu Val Cys Ile Asn Thr Leu Met Gln Gly Glu Gly Cys Val Gln Ser
145                 150                 155                 160
gtg gtg gaa agc atc gtt tat gcg gat agt ttt cat gac aca aaa aac   528
Val Val Glu Ser Ile Val Tyr Ala Asp Ser Phe His Asp Thr Lys Asn
                165                 170                 175
gct ttt gat gcg att gta gtg gct agg ggt ggg ggg agc atg gag gat   576
Ala Phe Asp Ala Ile Val Val Ala Arg Gly Gly Gly Ser Met Glu Asp
            180                 185                 190
ttg tat tct ttc aat gat gaa aaa atc gct gat gct ctg tat ttg gcc   624
Leu Tyr Ser Phe Asn Asp Glu Lys Ile Ala Asp Ala Leu Tyr Leu Ala
        195                 200                 205
aaa acc ttc agc atg tca gct att ggg cat gag agc gat ttt tta ttg   672
Lys Thr Phe Ser Met Ser Ala Ile Gly His Glu Ser Asp Phe Leu Leu
    210                 215                 220
agc gat tta gtg gcg gat tta agg gct tct acg cct tca aac gcg atg   720
Ser Asp Leu Val Ala Asp Leu Arg Ala Ser Thr Pro Ser Asn Ala Met
225                 230                 235                 240
gaa att tta ctc ccc agc agc gat gaa tgg ttg caa aga ctt gat ggg   768
Glu Ile Leu Leu Pro Ser Ser Asp Glu Trp Leu Gln Arg Leu Asp Gly
                245                 250                 255
ttt aat gtg aaa ttg cac cgc tcg ttt aaa act ttg ctc cac caa aaa   816
Phe Asn Val Lys Leu His Arg Ser Phe Lys Thr Leu Leu His Gln Lys
            260                 265                 270
aag gcg cat tta gag cat tta gtg gct tct tta aaa cga ttg agt ttt   864
Lys Ala His Leu Glu His Leu Val Ala Ser Leu Lys Arg Leu Ser Phe
        275                 280                 285
gaa aac aag cac cat tta aac gct tta aaa cta gaa aaa tta aaa atc   912
Glu Asn Lys His His Leu Asn Ala Leu Lys Leu Glu Lys Leu Lys Ile
    290                 295                 300
gcc cta gaa aat aaa act cta gaa ttt tta cgc ttt aaa aaa acg ctt   960
Ala Leu Glu Asn Lys Thr Leu Glu Phe Leu Arg Phe Lys Lys Thr Leu
305                 310                 315                 320
tta gaa aaa atc tct act caa aca tta aca agc cct ttt tta caa act  1008
Leu Glu Lys Ile Ser Thr Gln Thr Leu Thr Ser Pro Phe Leu Gln Thr
                325                 330                 335
aaa aca gag cga ttg aac agg cta                                  1032
Lys Thr Glu Arg Leu Asn Arg Leu
            340
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<210> 158

<211> 344
<212> PRT
<213> Helicobacter pylori
<400> 158

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Thr Phe Leu Gln Val Arg Val Gln Gly Glu Val Ser Asn Leu Thr Ile
 1               5                  10                  15
His Lys Val Ser Gly His Ala Tyr Phe Ser Leu Lys Asp Ser Gln Ser
            20                  25                  30
Val Ile Lys Cys Val Leu Phe Lys Gly Asn Ala Asn Arg Leu Lys Phe
        35                  40                  45
Ala Leu Lys Glu Gly Gln Glu Val Val Val Phe Gly Gly Ile Ser Val
    50                  55                  60
Tyr Val Pro Arg Gly Asp Tyr Gln Ile Asn Cys Phe Glu Ile Glu Pro
65                  70                  75                  80
Lys Asp Ile Gly Ser Leu Thr Leu Ala Leu Glu Gln Leu Lys Glu Lys
                85                  90                  95
Leu Arg Leu Lys Gly Tyr Phe Asp Glu Glu Asn Lys Leu Pro Lys Pro
            100                 105                 110
His Phe Pro Lys Arg Val Ala Val Ile Thr Ser Gln Asn Ser Ala Ala
        115                 120                 125
Trp Ala Asp Met Lys Lys Ile Ala Ser Lys Arg Trp Pro Met Cys Glu
    130                 135                 140
Leu Val Cys Ile Asn Thr Leu Met Gln Gly Glu Gly Cys Val Gln Ser
145                 150                 155                 160
Val Val Glu Ser Ile Val Tyr Ala Asp Ser Phe His Asp Thr Lys Asn
                165                 170                 175
Ala Phe Asp Ala Ile Val Val Ala Arg Gly Gly Gly Ser Met Glu Asp
            180                 185                 190
Leu Tyr Ser Phe Asn Asp Glu Lys Ile Ala Asp Ala Leu Tyr Leu Ala
        195                 200                 205
Lys Thr Phe Ser Met Ser Ala Ile Gly His Glu Ser Asp Phe Leu Leu
    210                 215                 220
Ser Asp Leu Val Ala Asp Leu Arg Ala Ser Thr Pro Ser Asn Ala Met
225                 230                 235                 240
Glu Ile Leu Leu Pro Ser Ser Asp Glu Trp Leu Gln Arg Leu Asp Gly
                245                 250                 255
Phe Asn Val Lys Leu His Arg Ser Phe Lys Thr Leu Leu His Gln Lys
            260                 265                 270
Lys Ala His Leu Glu His Leu Val Ala Ser Leu Lys Arg Leu Ser Phe
        275                 280                 285
Glu Asn Lys His His Leu Asn Ala Leu Lys Leu Glu Lys Leu Lys Ile
    290                 295                 300
Ala Leu Glu Asn Lys Thr Leu Glu Phe Leu Arg Phe Lys Lys Thr Leu
305                 310                 315                 320
Leu Glu Lys Ile Ser Thr Gln Thr Leu Thr Ser Pro Phe Leu Gln Thr
                325                 330                 335
Lys Thr Glu Arg Leu Asn Arg Leu
            340
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<210> 159
<211> 363
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(363)
<400> 159

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atc atc aaa ggc ggg ttc att gcg ttg agt caa atg ggt gac gcg aac   48
Ile Ile Lys Gly Gly Phe Ile Ala Leu Ser Gln Met Gly Asp Ala Asn
 1               5                  10                  15
gct tct atc cct acc cca caa cca gtt tat tac aga gaa atg ttc gct   96
Ala Ser Ile Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Ala
```

```
          20                  25                  30
cat cat ggt aaa gcc aaa tac gat gca aac atc act ttt gtg tct caa   144
His His Gly Lys Ala Lys Tyr Asp Ala Asn Ile Thr Phe Val Ser Gln
        35                  40                  45
gcg gct tat gac aaa ggc att aaa gaa gaa tta ggg ctt gaa aga caa   192
Ala Ala Tyr Asp Lys Gly Ile Lys Glu Glu Leu Gly Leu Glu Arg Gln
    50                  55                  60
gtg ttg ccg gta aaa aat tgc aga aac atc act aaa aaa gac atg caa   240
Val Leu Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Met Gln
65                  70                  75                  80
ttc aac gac act acc gct cac att gaa gtc aat cct gaa act tac cat   288
Phe Asn Asp Thr Thr Ala His Ile Glu Val Asn Pro Glu Thr Tyr His
                85                  90                  95
gtg ttc gtg gat ggc aaa gaa gta act tct aaa cca gcc aat aaa gtg   336
Val Phe Val Asp Gly Lys Glu Val Thr Ser Lys Pro Ala Asn Lys Val
            100                 105                 110
agc ttg gcg caa ctc ttt agc att ttc                             363
Ser Leu Ala Gln Leu Phe Ser Ile Phe
        115                 120
<210> 160
<211> 121
<212> PRT
<213> Helicobacter pylori
<400> 160
Ile Ile Lys Gly Gly Phe Ile Ala Leu Ser Gln Met Gly Asp Ala Asn
  1               5                  10                  15
Ala Ser Ile Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Ala
            20                  25                  30
His His Gly Lys Ala Lys Tyr Asp Ala Asn Ile Thr Phe Val Ser Gln
        35                  40                  45
Ala Ala Tyr Asp Lys Gly Ile Lys Glu Glu Leu Gly Leu Glu Arg Gln
    50                  55                  60
Val Leu Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Met Gln
65                  70                  75                  80
Phe Asn Asp Thr Thr Ala His Ile Glu Val Asn Pro Glu Thr Tyr His
                85                  90                  95
Val Phe Val Asp Gly Lys Glu Val Thr Ser Lys Pro Ala Asn Lys Val
            100                 105                 110
Ser Leu Ala Gln Leu Phe Ser Ile Phe
        115                 120
<210> 161
<211> 717
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(717)
<400> 161
cgg act aat aaa gcc ttg tat caa ttc att ttg aga ata gct caa aaa    48
Arg Thr Asn Lys Ala Leu Tyr Gln Phe Ile Leu Arg Ile Ala Gln Lys
  1               5                  10                  15
gac aat ttt gct tca gcg tat cta aca gtc aaa tta gaa tac cca caa    96
Asp Asn Phe Ala Ser Ala Tyr Leu Thr Val Lys Leu Glu Tyr Pro Gln
            20                  25                  30
aga cac gaa gtc tct agc gtt att gaa gag gag tta aaa aag aga gaa   144
Arg His Glu Val Ser Ser Val Ile Glu Glu Glu Leu Lys Lys Arg Glu
        35                  40                  45
gaa gca aag agg cag aaa gaa ttg att aag caa gaa aat ctt aac acc   192
Glu Ala Lys Arg Gln Lys Glu Leu Ile Lys Gln Glu Asn Leu Asn Thr
    50                  55                  60
aca gcc tac atc aat aga gtg atg atg gcg agc aat gaa cag att atc   240
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Thr Ala Tyr Ile Asn Arg Val Met Met Ala Ser Asn Glu Gln Ile Ile
 65                  70                  75                  80
aac aaa gaa aaa ata aga gaa gaa aag caa aaa att atc tta gat caa   288
Asn Lys Glu Lys Ile Arg Glu Glu Lys Gln Lys Ile Ile Leu Asp Gln
                 85                  90                  95
gca aag gcg cta gag act caa tat gtg cat aat gcc tta aaa aga aac   336
Ala Lys Ala Leu Glu Thr Gln Tyr Val His Asn Ala Leu Lys Arg Asn
            100                 105                 110
ccc gtg cct aga aac tac aac tac tac caa gcg cct gaa aaa cgc tct   384
Pro Val Pro Arg Asn Tyr Asn Tyr Tyr Gln Ala Pro Glu Lys Arg Ser
        115                 120                 125
aaa cat att atg ccc tct gaa att ttt gat gat ggc aca ttc act tat   432
Lys His Ile Met Pro Ser Glu Ile Phe Asp Asp Gly Thr Phe Thr Tyr
    130                 135                 140
ttt ggt ttc aaa aac atc act ctc caa cct gct att ttt gtg gtt caa   480
Phe Gly Phe Lys Asn Ile Thr Leu Gln Pro Ala Ile Phe Val Val Gln
145                 150                 155                 160
cct gat ggg aaa ttg agc atg act gat gcc gcc att gat cct aac atg   528
Pro Asp Gly Lys Leu Ser Met Thr Asp Ala Ala Ile Asp Pro Asn Met
                165                 170                 175
acc aat tca gga ttg aga tgg tat aga gtt aat gaa att gca gaa aaa   576
Thr Asn Ser Gly Leu Arg Trp Tyr Arg Val Asn Glu Ile Ala Glu Lys
            180                 185                 190
ttt aag ctc att aaa gac aaa gcc ctt gta aca gta atc aat aaa ggc   624
Phe Lys Leu Ile Lys Asp Lys Ala Leu Val Thr Val Ile Asn Lys Gly
        195                 200                 205
tat ggg aaa aat cca ttg aca aaa aat tac aat atc aaa aac tat ggt   672
Tyr Gly Lys Asn Pro Leu Thr Lys Asn Tyr Asn Ile Lys Asn Tyr Gly
    210                 215                 220
gaa ttg gag cgt gtg att aaa aag ctc cct ctt gtc aga gat aaa       717
Glu Leu Glu Arg Val Ile Lys Lys Leu Pro Leu Val Arg Asp Lys
225                 230                 235
<210> 162
<211> 239
<212> PRT
<213> Helicobacter pylori
<400> 162
Arg Thr Asn Lys Ala Leu Tyr Gln Phe Ile Leu Arg Ile Ala Gln Lys
  1               5                  10                  15
Asp Asn Phe Ala Ser Ala Tyr Leu Thr Val Lys Leu Glu Tyr Pro Gln
             20                  25                  30
Arg His Glu Val Ser Ser Val Ile Glu Glu Glu Leu Lys Lys Arg Glu
         35                  40                  45
Glu Ala Lys Arg Gln Lys Glu Leu Ile Lys Gln Glu Asn Leu Asn Thr
     50                  55                  60
Thr Ala Tyr Ile Asn Arg Val Met Met Ala Ser Asn Glu Gln Ile Ile
 65                  70                  75                  80
Asn Lys Glu Lys Ile Arg Glu Glu Lys Gln Lys Ile Ile Leu Asp Gln
                 85                  90                  95
Ala Lys Ala Leu Glu Thr Gln Tyr Val His Asn Ala Leu Lys Arg Asn
            100                 105                 110
Pro Val Pro Arg Asn Tyr Asn Tyr Tyr Gln Ala Pro Glu Lys Arg Ser
        115                 120                 125
Lys His Ile Met Pro Ser Glu Ile Phe Asp Asp Gly Thr Phe Thr Tyr
    130                 135                 140
Phe Gly Phe Lys Asn Ile Thr Leu Gln Pro Ala Ile Phe Val Val Gln
145                 150                 155                 160
Pro Asp Gly Lys Leu Ser Met Thr Asp Ala Ala Ile Asp Pro Asn Met
                165                 170                 175
Thr Asn Ser Gly Leu Arg Trp Tyr Arg Val Asn Glu Ile Ala Glu Lys
            180                 185                 190
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Phe Lys Leu Ile Lys Asp Lys Ala Leu Val Thr Val Ile Asn Lys Gly
        195                 200                 205
Tyr Gly Lys Asn Pro Leu Thr Lys Asn Tyr Asn Ile Lys Asn Tyr Gly
    210                 215                 220
Glu Leu Glu Arg Val Ile Lys Lys Leu Pro Leu Val Arg Asp Lys
225                 230                 235
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<211> 1077
<212> DNA
<213> Helicobacter pylori
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<221> CDS
<222> (1)..(1077)
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gaa ggc act aaa gag ctt ggt gcg gtg ggg ttt gcg caa ctt tta gag   48
Glu Gly Thr Lys Glu Leu Gly Ala Val Gly Phe Ala Gln Leu Leu Glu
  1               5                  10                  15
caa aaa gcg atc agt ttg aat gtg gat acc agc aca gaa gat ttg caa   96
Gln Lys Ala Ile Ser Leu Asn Val Asp Thr Ser Thr Glu Asp Leu Gln
            20                  25                  30
atc act tta gaa ttt tta aaa gaa tac gaa gat gaa gcc att acg cgc   144
Ile Thr Leu Glu Phe Leu Lys Glu Tyr Glu Asp Glu Ala Ile Thr Arg
        35                  40                  45
tta aaa gag ctt tta aaa tcc cct aat ttc acg caa aac gct tta gaa   192
Leu Lys Glu Leu Leu Lys Ser Pro Asn Phe Thr Gln Asn Ala Leu Glu
    50                  55                  60
aaa gtc aaa acc caa atg tta gcc gca ctt tta caa aaa gaa agc gat   240
Lys Val Lys Thr Gln Met Leu Ala Ala Leu Leu Gln Lys Glu Ser Asp
65                  70                  75                  80
ttt gac tat ttg gct aaa ttg act tta aag caa gag ctt ttt gct aac   288
Phe Asp Tyr Leu Ala Lys Leu Thr Leu Lys Gln Glu Leu Phe Ala Asn
                85                  90                  95
acc cct tta gct aac gca gcc tta ggc act aaa gag agc att caa aaa   336
Thr Pro Leu Ala Asn Ala Ala Leu Gly Thr Lys Glu Ser Ile Gln Lys
            100                 105                 110
atc aag cta gac gat ttg aaa cag caa ttt gct aag gtc ttt gaa ctc   384
Ile Lys Leu Asp Asp Leu Lys Gln Gln Phe Ala Lys Val Phe Glu Leu
        115                 120                 125
aat aag ctc gtg gtg gtg ctt ggg ggc gat ttg aaa atc gat caa acc   432
Asn Lys Leu Val Val Val Leu Gly Gly Asp Leu Lys Ile Asp Gln Thr
    130                 135                 140
ctt aag cgt ttg aat aac gcc ctt aat ttc ttg cca caa ggt aaa gcg   480
Leu Lys Arg Leu Asn Asn Ala Leu Asn Phe Leu Pro Gln Gly Lys Ala
145                 150                 155                 160
tat gaa gag cct tat ttt gaa acg agc gat aaa aaa agc gaa aaa gtc   528
Tyr Glu Glu Pro Tyr Phe Glu Thr Ser Asp Lys Lys Ser Glu Lys Val
                165                 170                 175
ctc tat aaa gac act gag cag gct ttc gtg tat ttt ggt gcg ccc ttt   576
Leu Tyr Lys Asp Thr Glu Gln Ala Phe Val Tyr Phe Gly Ala Pro Phe
            180                 185                 190
aaa atc aag gat tta aaa cag gat tta gcg aaa tct aaa gtc atg atg   624
Lys Ile Lys Asp Leu Lys Gln Asp Leu Ala Lys Ser Lys Val Met Met
        195                 200                 205
ttt gtg ctt ggt ggg ggg ttt ggc tct cgt tta atg gaa aaa atc agg   672
Phe Val Leu Gly Gly Gly Phe Gly Ser Arg Leu Met Glu Lys Ile Arg
    210                 215                 220
gtt caa gag gga tta gct tat agc gtg tat atc cgc tcc aat ttt tct   720
Val Gln Glu Gly Leu Ala Tyr Ser Val Tyr Ile Arg Ser Asn Phe Ser
225                 230                 235                 240
aaa gtg gcg cat ttt gcg agc ggg tat ttg caa acc aag ctc agc act   768
Lys Val Ala His Phe Ala Ser Gly Tyr Leu Gln Thr Lys Leu Ser Thr
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                245                 250                 255
caa act aaa agc gtt gcc tta gtt aaa aaa atc gtt aag gaa ttt ata   816
Gln Thr Lys Ser Val Ala Leu Val Lys Lys Ile Val Lys Glu Phe Ile
            260                 265                 270
gaa aaa ggc atg acg caa caa gaa tta gac gac gct aaa aag ttt tta   864
Glu Lys Gly Met Thr Gln Gln Glu Leu Asp Asp Ala Lys Lys Phe Leu
        275                 280                 285
cta ggc tct gag cct tta agg aat gaa acg atc tct agc cgc ttg aac   912
Leu Gly Ser Glu Pro Leu Arg Asn Glu Thr Ile Ser Ser Arg Leu Asn
    290                 295                 300
acc act tac aat tat ttt tat tta ggt ttg cct tta aat ttt aac caa   960
Thr Thr Tyr Asn Tyr Phe Tyr Leu Gly Leu Pro Leu Asn Phe Asn Gln
305                 310                 315                 320
acg ctg ctc aat caa atc caa aaa atg agt ttg aaa gaa atc aat gat  1008
Thr Leu Leu Asn Gln Ile Gln Lys Met Ser Leu Lys Glu Ile Asn Asp
                325                 330                 335
ttc att aaa gcc cac acc gaa atc aac gac ttg act ttt gct att gtg  1056
Phe Ile Lys Ala His Thr Glu Ile Asn Asp Leu Thr Phe Ala Ile Val
            340                 345                 350
agc aat aaa aag aag gac aaa                                     1077
Ser Asn Lys Lys Lys Asp Lys
        355
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<211> 359
<212> PRT
<213> Helicobacter pylori
<400> 164
Glu Gly Thr Lys Glu Leu Gly Ala Val Gly Phe Ala Gln Leu Leu Glu
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Gln Lys Ala Ile Ser Leu Asn Val Asp Thr Ser Thr Glu Asp Leu Gln
             20                  25                  30
Ile Thr Leu Glu Phe Leu Lys Glu Tyr Glu Asp Glu Ala Ile Thr Arg
         35                  40                  45
Leu Lys Glu Leu Leu Lys Ser Pro Asn Phe Thr Gln Asn Ala Leu Glu
     50                  55                  60
Lys Val Lys Thr Gln Met Leu Ala Ala Leu Leu Gln Lys Glu Ser Asp
 65                  70                  75                  80
Phe Asp Tyr Leu Ala Lys Leu Thr Leu Lys Gln Glu Leu Phe Ala Asn
                 85                  90                  95
Thr Pro Leu Ala Asn Ala Ala Leu Gly Thr Lys Glu Ser Ile Gln Lys
            100                 105                 110
Ile Lys Leu Asp Asp Leu Lys Gln Gln Phe Ala Lys Val Phe Glu Leu
        115                 120                 125
Asn Lys Leu Val Val Val Leu Gly Gly Asp Leu Lys Ile Asp Gln Thr
    130                 135                 140
Leu Lys Arg Leu Asn Asn Ala Leu Asn Phe Leu Pro Gln Gly Lys Ala
145                 150                 155                 160
Tyr Glu Glu Pro Tyr Phe Glu Thr Ser Asp Lys Lys Ser Glu Lys Val
                165                 170                 175
Leu Tyr Lys Asp Thr Glu Gln Ala Phe Val Tyr Phe Gly Ala Pro Phe
            180                 185                 190
Lys Ile Lys Asp Leu Lys Gln Asp Leu Ala Lys Ser Lys Val Met Met
        195                 200                 205
Phe Val Leu Gly Gly Gly Phe Gly Ser Arg Leu Met Glu Lys Ile Arg
    210                 215                 220
Val Gln Glu Gly Leu Ala Tyr Ser Val Tyr Ile Arg Ser Asn Phe Ser
225                 230                 235                 240
Lys Val Ala His Phe Ala Ser Gly Tyr Leu Gln Thr Lys Leu Ser Thr
                245                 250                 255
Gln Thr Lys Ser Val Ala Leu Val Lys Lys Ile Val Lys Glu Phe Ile
            260                 265                 270
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Glu Lys Gly Met Thr Gln Gln Glu Leu Asp Asp Ala Lys Lys Phe Leu
        275                 280                 285
Leu Gly Ser Glu Pro Leu Arg Asn Glu Thr Ile Ser Ser Arg Leu Asn
    290                 295                 300
Thr Thr Tyr Asn Tyr Phe Tyr Leu Gly Leu Pro Leu Asn Phe Asn Gln
305                 310                 315                 320
Thr Leu Leu Asn Gln Ile Gln Lys Met Ser Leu Lys Glu Ile Asn Asp
                325                 330                 335
Phe Ile Lys Ala His Thr Glu Ile Asn Asp Leu Thr Phe Ala Ile Val
            340                 345                 350
Ser Asn Lys Lys Lys Asp Lys
        355
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<211> 882
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<222> (1)..(882)
<400> 165
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Glu Glu Asp Gly Asn Glu Ser Ile Ala Tyr Asp Phe Ser Ser Ala Lys
  1               5                  10                  15
gag ttg cta gaa ttg tgc caa aaa cac caa aaa agc atc gct gaa atc   96
Glu Leu Leu Glu Leu Cys Gln Lys His Gln Lys Ser Ile Ala Glu Ile
            20                  25                  30
gtg cgt ttg aga gaa aac gcc ctg aaa aac cac cct gat gca acg atg   144
Val Arg Leu Arg Glu Asn Ala Leu Lys Asn His Pro Asp Ala Thr Met
        35                  40                  45
gtt aaa att tat cat gcg atg ctt gag tgt tat gat aat ggg gct aat   192
Val Lys Ile Tyr His Ala Met Leu Glu Cys Tyr Asp Asn Gly Ala Asn
    50                  55                  60
tct aaa gaa agg tat ctg cct ggt tct ttg aaa gta aca cga ttg gcc   240
Ser Lys Glu Arg Tyr Leu Pro Gly Ser Leu Lys Val Thr Arg Leu Ala
65                  70                  75                  80
cca agc att aaa acg cgc cta gaa aaa cac ccc aca agc ggg aaa gac   288
Pro Ser Ile Lys Thr Arg Leu Glu Lys His Pro Thr Ser Gly Lys Asp
                85                  90                  95
ccc tta gcc ttg att gat tac att tcg ctt tac gct cgc gcc att gct   336
Pro Leu Ala Leu Ile Asp Tyr Ile Ser Leu Tyr Ala Arg Ala Ile Ala
            100                 105                 110
gaa gaa aac gct agc gga ggc aag gtg gta acc gcc ccc act aat ggg   384
Glu Glu Asn Ala Ser Gly Gly Lys Val Val Thr Ala Pro Thr Asn Gly
        115                 120                 125
gcg tgc gcg gtg gtg cca agc gtg ctt tta tac gct aaa aac cat ttg   432
Ala Cys Ala Val Val Pro Ser Val Leu Leu Tyr Ala Lys Asn His Leu
    130                 135                 140
ttt gaa aat tta tcg caa aag gct atc aat gat ttt tta ctc act agt   480
Phe Glu Asn Leu Ser Gln Lys Ala Ile Asn Asp Phe Leu Leu Thr Ser
145                 150                 155                 160
gcg gcg att ggc tat ctt tac aag aaa aac gct tcc ttg agt ggc gca   528
Ala Ala Ile Gly Tyr Leu Tyr Lys Lys Asn Ala Ser Leu Ser Gly Ala
                165                 170                 175
gaa gcc ggg tgt cag gct gaa att ggc gtg gca agc tct atg gct gcg   576
Glu Ala Gly Cys Gln Ala Glu Ile Gly Val Ala Ser Ser Met Ala Ala
            180                 185                 190
ggg ggg tta gct cat ttg tgc caa gcg acc acg caa cag gtt ttg atc   624
Gly Gly Leu Ala His Leu Cys Gln Ala Thr Thr Gln Gln Val Leu Ile
        195                 200                 205
gct agt gaa atc gct atg gaa cac cat tta gga ttg aca tgc gat ccg   672
Ala Ser Glu Ile Ala Met Glu His His Leu Gly Leu Thr Cys Asp Pro
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    210                 215                 220
gtg ggg ggc ttg gtg caa atc cct tgc att gaa cgc aat gtt tta ggg   720
Val Gly Gly Leu Val Gln Ile Pro Cys Ile Glu Arg Asn Val Leu Gly
225                 230                 235                 240
gcg att aaa gcg atc agc gct tct aaa cta gcc tta gaa gat gaa tac   768
Ala Ile Lys Ala Ile Ser Ala Ser Lys Leu Ala Leu Glu Asp Glu Tyr
                245                 250                 255
aag cct aaa gtg agt ctg gat gaa gtg atc gct aca atg tat gcg acc   816
Lys Pro Lys Val Ser Leu Asp Glu Val Ile Ala Thr Met Tyr Ala Thr
            260                 265                 270
gga aaa gac atg aat gaa aaa tac aaa gag act tcg tta ggg ggg tta   864
Gly Lys Asp Met Asn Glu Lys Tyr Lys Glu Thr Ser Leu Gly Gly Leu
        275                 280                 285
gcc aaa acc tta aaa tgc                                          882
Ala Lys Thr Leu Lys Cys
    290
<210> 166
<211> 294
<212> PRT
<213> Helicobacter pylori
<400> 166
Glu Glu Asp Gly Asn Glu Ser Ile Ala Tyr Asp Phe Ser Ser Ala Lys
  1               5                  10                  15
Glu Leu Leu Glu Leu Cys Gln Lys His Gln Lys Ser Ile Ala Glu Ile
            20                  25                  30
Val Arg Leu Arg Glu Asn Ala Leu Lys Asn His Pro Asp Ala Thr Met
        35                  40                  45
Val Lys Ile Tyr His Ala Met Leu Glu Cys Tyr Asp Asn Gly Ala Asn
    50                  55                  60
Ser Lys Glu Arg Tyr Leu Pro Gly Ser Leu Lys Val Thr Arg Leu Ala
65                  70                  75                  80
Pro Ser Ile Lys Thr Arg Leu Glu Lys His Pro Thr Ser Gly Lys Asp
                85                  90                  95
Pro Leu Ala Leu Ile Asp Tyr Ile Ser Leu Tyr Ala Arg Ala Ile Ala
            100                 105                 110
Glu Glu Asn Ala Ser Gly Gly Lys Val Val Thr Ala Pro Thr Asn Gly
        115                 120                 125
Ala Cys Ala Val Val Pro Ser Val Leu Leu Tyr Ala Lys Asn His Leu
    130                 135                 140
Phe Glu Asn Leu Ser Gln Lys Ala Ile Asn Asp Phe Leu Leu Thr Ser
145                 150                 155                 160
Ala Ala Ile Gly Tyr Leu Tyr Lys Lys Asn Ala Ser Leu Ser Gly Ala
                165                 170                 175
Glu Ala Gly Cys Gln Ala Glu Ile Gly Val Ala Ser Ser Met Ala Ala
            180                 185                 190
Gly Gly Leu Ala His Leu Cys Gln Ala Thr Thr Gln Gln Val Leu Ile
        195                 200                 205
Ala Ser Glu Ile Ala Met Glu His His Leu Gly Leu Thr Cys Asp Pro
    210                 215                 220
Val Gly Gly Leu Val Gln Ile Pro Cys Ile Glu Arg Asn Val Leu Gly
225                 230                 235                 240
Ala Ile Lys Ala Ile Ser Ala Ser Lys Leu Ala Leu Glu Asp Glu Tyr
                245                 250                 255
Lys Pro Lys Val Ser Leu Asp Glu Val Ile Ala Thr Met Tyr Ala Thr
            260                 265                 270
Gly Lys Asp Met Asn Glu Lys Tyr Lys Glu Thr Ser Leu Gly Gly Leu
        275                 280                 285
Ala Lys Thr Leu Lys Cys
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<210> 167
<211> 177
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<213> Helicobacter pylori
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<222> (1)..(177)
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1 5 10 15
aaa ttg agc gat ttt aac gaa gaa gaa ttg aaa atc atg ttt gaa gcg 96
Lys Leu Ser Asp Phe Asn Glu Glu Glu Leu Lys Ile Met Phe Glu Ala
20 25 30
gaa gag aaa agg ctt tta gaa caa atc caa act aag cat ttt aaa gaa 144
Glu Glu Lys Arg Leu Leu Glu Gln Ile Gln Thr Lys His Phe Lys Glu
35 40 45
gtt tgg gaa aag ggc gac aat gag caa gga aaa 177
Val Trp Glu Lys Gly Asp Asn Glu Gln Gly Lys
50 55
<210> 168
<211> 59
<212> PRT
<213> Helicobacter pylori
<400> 168
Glu Gln Ala Val Lys Ile Val Glu Lys Arg Leu Lys Lys Glu Gly Met
1 5 10 15
Lys Leu Ser Asp Phe Asn Glu Glu Glu Leu Lys Ile Met Phe Glu Ala
20 25 30
Glu Glu Lys Arg Leu Leu Glu Gln Ile Gln Thr Lys His Phe Lys Glu
35 40 45
Val Trp Glu Lys Gly Asp Asn Glu Gln Gly Lys
50 55
<210> 169
<211> 971
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<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(969)
<400> 169
gtt atc act aat cgt gga ggg cgc act tgc cat gcc gct att gtg gcg 48
Val Ile Thr Asn Arg Gly Gly Arg Thr Cys His Ala Ala Ile Val Ala
1 5 10 15
aga gaa att ggc gtg cca gct atc gtt ggg gtg agc ggg gcg act gat 96
Arg Glu Ile Gly Val Pro Ala Ile Val Gly Val Ser Gly Ala Thr Asp
20 25 30
agc ctt tat acc ggc atg gaa atc acg gtt tct tgc gct gag ggc gaa 144
Ser Leu Tyr Thr Gly Met Glu Ile Thr Val Ser Cys Ala Glu Gly Glu
35 40 45
gag ggc tat gtg tat gcg ggc att tat gag cat gaa att gaa agg gtg 192
Glu Gly Tyr Val Tyr Ala Gly Ile Tyr Glu His Glu Ile Glu Arg Val
50 55 60
gag ctt tct aac atg caa gaa act caa aca aaa att tac atc aat att 240
Glu Leu Ser Asn Met Gln Glu Thr Gln Thr Lys Ile Tyr Ile Asn Ile
65 70 75 80
gga aac cct gaa aaa gcc ttt ggc ttt tct caa ctc cct aat cac ggc 288
Gly Asn Pro Glu Lys Ala Phe Gly Phe Ser Gln Leu Pro Asn His Gly
85 90 95
gta ggg cta gcc agg atg gaa atg att att tta aat caa atc aaa gcc 336
Val Gly Leu Ala Arg Met Glu Met Ile Ile Leu Asn Gln Ile Lys Ala
100 105 110
cac cct tta gct tta gtg gat ttg cac cac aaa aaa agc gtg aaa gaa 384

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His Pro Leu Ala Leu Val Asp Leu His His Lys Lys Ser Val Lys Glu
        115                 120                 125
aaa aat gaa att gaa aac ctc atg gca ggc tat gct aac cct aaa gat   432
Lys Asn Glu Ile Glu Asn Leu Met Ala Gly Tyr Ala Asn Pro Lys Asp
    130                 135                 140
ttt ttt gtg aaa aaa atc gct gaa ggc att ggc atg atc agt gca gcg   480
Phe Phe Val Lys Lys Ile Ala Glu Gly Ile Gly Met Ile Ser Ala Ala
145                 150                 155                 160
ttt tac cct aaa cct gtc att gtg aga acg agc gat ttc aaa tcc aat   528
Phe Tyr Pro Lys Pro Val Ile Val Arg Thr Ser Asp Phe Lys Ser Asn
                165                 170                 175
gaa tac atg cgc atg ctt ggc ggc tct agc tat gag cct aat gaa gaa   576
Glu Tyr Met Arg Met Leu Gly Gly Ser Ser Tyr Glu Pro Asn Glu Glu
            180                 185                 190
aac ccc atg ctt ggc tat agg ggg gct agt cgg tat tat tca gag agc   624
Asn Pro Met Leu Gly Tyr Arg Gly Ala Ser Arg Tyr Tyr Ser Glu Ser
        195                 200                 205
tat aat gaa gcg ttt tcg tgg gag tgt gaa gcc tta gcg tta gtg agg   672
Tyr Asn Glu Ala Phe Ser Trp Glu Cys Glu Ala Leu Ala Leu Val Arg
    210                 215                 220
gaa gaa atg gga tta acc aac atg aaa gtg atg atc cct ttt ttg cga   720
Glu Glu Met Gly Leu Thr Asn Met Lys Val Met Ile Pro Phe Leu Arg
225                 230                 235                 240
acc att gaa gag ggt aaa aaa gtc cta gaa atc tta aga aaa aac aat   768
Thr Ile Glu Glu Gly Lys Lys Val Leu Glu Ile Leu Arg Lys Asn Asn
                245                 250                 255
tta gaa tcc ggt aaa aac ggg ctt gaa att tat atc atg tgc gaa ttg   816
Leu Glu Ser Gly Lys Asn Gly Leu Glu Ile Tyr Ile Met Cys Glu Leu
            260                 265                 270
ccg gtg aat gtc att ttg gct gat gat ttc ttg agc ttg ttt gat ggc   864
Pro Val Asn Val Ile Leu Ala Asp Asp Phe Leu Ser Leu Phe Asp Gly
        275                 280                 285
ttt tct att gga tca aac gat tta acc cag ctc act tta ggc gtg gat   912
Phe Ser Ile Gly Ser Asn Asp Leu Thr Gln Leu Thr Leu Gly Val Asp
    290                 295                 300
aga gac agc gaa ttg gtc agc cat gtc ttt gat gaa agg aat gaa gcg   960
Arg Asp Ser Glu Leu Val Ser His Val Phe Asp Glu Arg Asn Glu Ala
305                 310                 315                 320
atg cta aag at                                                   971
Met Leu Lys
<210> 170
<211> 323
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<213> Helicobacter pylori
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Val Ile Thr Asn Arg Gly Gly Arg Thr Cys His Ala Ala Ile Val Ala
  1               5                  10                  15
Arg Glu Ile Gly Val Pro Ala Ile Val Gly Val Ser Gly Ala Thr Asp
            20                  25                  30
Ser Leu Tyr Thr Gly Met Glu Ile Thr Val Ser Cys Ala Glu Gly Glu
        35                  40                  45
Glu Gly Tyr Val Tyr Ala Gly Ile Tyr Glu His Glu Ile Glu Arg Val
    50                  55                  60
Glu Leu Ser Asn Met Gln Glu Thr Gln Thr Lys Ile Tyr Ile Asn Ile
65                  70                  75                  80
Gly Asn Pro Glu Lys Ala Phe Gly Phe Ser Gln Leu Pro Asn His Gly
                85                  90                  95
Val Gly Leu Ala Arg Met Glu Met Ile Ile Leu Asn Gln Ile Lys Ala
            100                 105                 110
His Pro Leu Ala Leu Val Asp Leu His His Lys Lys Ser Val Lys Glu
        115                 120                 125
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Lys Asn Glu Ile Glu Asn Leu Met Ala Gly Tyr Ala Asn Pro Lys Asp
    130                 135                 140
Phe Phe Val Lys Lys Ile Ala Glu Gly Ile Gly Met Ile Ser Ala Ala
145                 150                 155                 160
Phe Tyr Pro Lys Pro Val Ile Val Arg Thr Ser Asp Phe Lys Ser Asn
                165                 170                 175
Glu Tyr Met Arg Met Leu Gly Gly Ser Ser Tyr Glu Pro Asn Glu Glu
            180                 185                 190
Asn Pro Met Leu Gly Tyr Arg Gly Ala Ser Arg Tyr Tyr Ser Glu Ser
        195                 200                 205
Tyr Asn Glu Ala Phe Ser Trp Glu Cys Glu Ala Leu Ala Leu Val Arg
    210                 215                 220
Glu Glu Met Gly Leu Thr Asn Met Lys Val Met Ile Pro Phe Leu Arg
225                 230                 235                 240
Thr Ile Glu Glu Gly Lys Lys Val Leu Glu Ile Leu Arg Lys Asn Asn
                245                 250                 255
Leu Glu Ser Gly Lys Asn Gly Leu Glu Ile Tyr Ile Met Cys Glu Leu
            260                 265                 270
Pro Val Asn Val Ile Leu Ala Asp Asp Phe Leu Ser Leu Phe Asp Gly
        275                 280                 285
Phe Ser Ile Gly Ser Asn Asp Leu Thr Gln Leu Thr Leu Gly Val Asp
    290                 295                 300
Arg Asp Ser Glu Leu Val Ser His Val Phe Asp Glu Arg Asn Glu Ala
305                 310                 315                 320
Met Leu Lys
<210> 171
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<213> Helicobacter pylori
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<222> (1)..(459)
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att tta gcg gac gac aga gcc acg act tta gag gtg atg gcc tat cac   48
Ile Leu Ala Asp Asp Arg Ala Thr Thr Leu Glu Val Met Ala Tyr His
  1               5                  10                  15
atg gaa gaa tta gaa tta aaa gat gaa gat att gcg tgt tgt ttg tat   96
Met Glu Glu Leu Glu Leu Lys Asp Glu Asp Ile Ala Cys Cys Leu Tyr
             20                  25                  30
ggc gct tca gcg ctt tta caa gaa aag cat tta aaa aac gct ttt gaa   144
Gly Ala Ser Ala Leu Leu Gln Glu Lys His Leu Lys Asn Ala Phe Glu
         35                  40                  45
act tta aac aaa aac caa aat acg gat tat gtt ttc aca tgc tct cca   192
Thr Leu Asn Lys Asn Gln Asn Thr Asp Tyr Val Phe Thr Cys Ser Pro
     50                  55                  60
ttt agc gct tcg ccc tat cgt tct ttt agt ctt gaa aac ggc gtt caa   240
Phe Ser Ala Ser Pro Tyr Arg Ser Phe Ser Leu Glu Asn Gly Val Gln
 65                  70                  75                  80
atg gct ttt aaa gag cat tca aac acg cgc acg caa gat tta aaa acg   288
Met Ala Phe Lys Glu His Ser Asn Thr Arg Thr Gln Asp Leu Lys Thr
                 85                  90                  95
ctc tat cat gac gcg ggg ttg ctt tat atg ggg aag gct caa gcc ttt   336
Leu Tyr His Asp Ala Gly Leu Leu Tyr Met Gly Lys Ala Gln Ala Phe
            100                 105                 110
aaa gaa atg cgg cct att ttt agt caa aat tct atc gct tta gaa tta   384
Lys Glu Met Arg Pro Ile Phe Ser Gln Asn Ser Ile Ala Leu Glu Leu
        115                 120                 125
tcg ccc tta gaa gtc caa gat att gca cac ttt aga aga ttt aga att   432
Ser Pro Leu Glu Val Gln Asp Ile Ala His Phe Arg Arg Phe Arg Ile
    130                 135                 140
agc caa gct caa ata cag ccg ttt gaa                              459
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Ser Gln Ala Gln Ile Gln Pro Phe Glu
145                 150
<210> 172
<211> 153
<212> PRT
<213> Helicobacter pylori
<400> 172
Ile Leu Ala Asp Asp Arg Ala Thr Thr Leu Glu Val Met Ala Tyr His
  1               5                  10                  15
Met Glu Glu Leu Glu Leu Lys Asp Glu Asp Ile Ala Cys Cys Leu Tyr
            20                  25                  30
Gly Ala Ser Ala Leu Leu Gln Glu Lys His Leu Lys Asn Ala Phe Glu
        35                  40                  45
Thr Leu Asn Lys Asn Gln Asn Thr Asp Tyr Val Phe Thr Cys Ser Pro
    50                  55                  60
Phe Ser Ala Ser Pro Tyr Arg Ser Phe Ser Leu Glu Asn Gly Val Gln
65                  70                  75                  80
Met Ala Phe Lys Glu His Ser Asn Thr Arg Thr Gln Asp Leu Lys Thr
                85                  90                  95
Leu Tyr His Asp Ala Gly Leu Leu Tyr Met Gly Lys Ala Gln Ala Phe
            100                 105                 110
Lys Glu Met Arg Pro Ile Phe Ser Gln Asn Ser Ile Ala Leu Glu Leu
        115                 120                 125
Ser Pro Leu Glu Val Gln Asp Ile Ala His Phe Arg Arg Phe Arg Ile
    130                 135                 140
Ser Gln Ala Gln Ile Gln Pro Phe Glu
145                 150
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<222> (1)..(432)
<400> 173
gag cag aaa ttc act gaa tct aag agt tac atg gaa tgg att aaa ggc   48
Glu Gln Lys Phe Thr Glu Ser Lys Ser Tyr Met Glu Trp Ile Lys Gly
  1               5                  10                  15
ctt tat gaa aaa agc gat ggc cct act ttg aaa tcg ttt gat cag ttt   96
Leu Tyr Glu Lys Ser Asp Gly Pro Thr Leu Lys Ser Phe Asp Gln Phe
            20                  25                  30
tgg agg gat ggt ttt gtg gag ttt gaa atc cct gaa aat gcg aga aag   144
Trp Arg Asp Gly Phe Val Glu Phe Glu Ile Pro Glu Asn Ala Arg Lys
        35                  40                  45
ttt gtg cgt cat gcg aaa ttc agg caa gac cct att aac aat aag ctg   192
Phe Val Arg His Ala Lys Phe Arg Gln Asp Pro Ile Asn Asn Lys Leu
    50                  55                  60
gat aca gag agt ggg aaa att caa att ttt tct caa aaa tgc gcg gat   240
Asp Thr Glu Ser Gly Lys Ile Gln Ile Phe Ser Gln Lys Cys Ala Asp
65                  70                  75                  80
ttt aaa ctg gcc gat ttt aaa ggg cat cct act tgg ttt gag cca gct   288
Phe Lys Leu Ala Asp Phe Lys Gly His Pro Thr Trp Phe Glu Pro Ala
                85                  90                  95
gag tgg cta ggc tct aaa atg gct gag att tat ccg ttc cat tta atc   336
Glu Trp Leu Gly Ser Lys Met Ala Glu Ile Tyr Pro Phe His Leu Ile
            100                 105                 110
tct ccg cac cca aaa tac cgt gtc aat tca cag ctt gat aac act tgg   384
Ser Pro His Pro Lys Tyr Arg Val Asn Ser Gln Leu Asp Asn Thr Trp
        115                 120                 125
gtt agg aat gtg tat aaa att caa ggc aga gag cct gta atg atc aat   432
Val Arg Asn Val Tyr Lys Ile Gln Gly Arg Glu Pro Val Met Ile Asn
```

130 135 140

<210> 174
<211> 144
<212> PRT
<213> Helicobacter pylori
<400> 174

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Glu Gln Lys Phe Thr Glu Ser Lys Ser Tyr Met Glu Trp Ile Lys Gly
 1               5                  10                  15
Leu Tyr Glu Lys Ser Asp Gly Pro Thr Leu Lys Ser Phe Asp Gln Phe
            20                  25                  30
Trp Arg Asp Gly Phe Val Glu Phe Glu Ile Pro Glu Asn Ala Arg Lys
        35                  40                  45
Phe Val Arg His Ala Lys Phe Arg Gln Asp Pro Ile Asn Asn Lys Leu
    50                  55                  60
Asp Thr Glu Ser Gly Lys Ile Gln Ile Phe Ser Gln Lys Cys Ala Asp
65                  70                  75                  80
Phe Lys Leu Ala Asp Phe Lys Gly His Pro Thr Trp Phe Glu Pro Ala
                85                  90                  95
Glu Trp Leu Gly Ser Lys Met Ala Glu Ile Tyr Pro Phe His Leu Ile
            100                 105                 110
Ser Pro His Pro Lys Tyr Arg Val Asn Ser Gln Leu Asp Asn Thr Trp
        115                 120                 125
Val Arg Asn Val Tyr Lys Ile Gln Gly Arg Glu Pro Val Met Ile Asn
    130                 135                 140
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<210> 175
<211> 1117
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(1116)
<400> 175

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cgc acg ctt gaa ttg agc ggc tat gaa gtg atg cta gta agg aat ttc   48
Arg Thr Leu Glu Leu Ser Gly Tyr Glu Val Met Leu Val Arg Asn Phe
 1               5                  10                  15
aca gat att gac gat aag atc atc aac aaa gcc cta aaa gaa aac aaa   96
Thr Asp Ile Asp Asp Lys Ile Ile Asn Lys Ala Leu Lys Glu Asn Lys
            20                  25                  30
agc att caa gaa tta agc agc att tat att gaa tct tac acg agg gat  144
Ser Ile Gln Glu Leu Ser Ser Ile Tyr Ile Glu Ser Tyr Thr Arg Asp
        35                  40                  45
ttg aac gct ttg aac gtg aaa aaa ccc agc cta gag cct aaa gcg agc  192
Leu Asn Ala Leu Asn Val Lys Lys Pro Ser Leu Glu Pro Lys Ala Ser
    50                  55                  60
gag tat tta gac gct atg gtg ggc atg att gaa acg ctt tta gaa aaa  240
Glu Tyr Leu Asp Ala Met Val Gly Met Ile Glu Thr Leu Leu Glu Lys
65                  70                  75                  80
aat atc gct tat cag gtc tct aat ggg gat att tat tta gac acg agc  288
Asn Ile Ala Tyr Gln Val Ser Asn Gly Asp Ile Tyr Leu Asp Thr Ser
                85                  90                  95
aag gat aaa gat tac ggc tct ttg agc gtg cat aat agc agc att gaa  336
Lys Asp Lys Asp Tyr Gly Ser Leu Ser Val His Asn Ser Ser Ile Glu
            100                 105                 110
ttt ggc cgt att ggt ttg gtg caa gaa aaa cgg ctt gag cag gat ttt  384
Phe Gly Arg Ile Gly Leu Val Gln Glu Lys Arg Leu Glu Gln Asp Phe
        115                 120                 125
gtg tta tgg aaa agc tat aag ggg gat aat gat gtg ggc ttt gat agc  432
Val Leu Trp Lys Ser Tyr Lys Gly Asp Asn Asp Val Gly Phe Asp Ser
    130                 135                 140
cct tta ggc aaa ggg cgc cct ggc tgg cat ata gaa tgc tct agc atg  480
Pro Leu Gly Lys Gly Arg Pro Gly Trp His Ile Glu Cys Ser Ser Met
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145                 150                 155                 160
gtt ttt gaa act tta gcg ctc act aac acc ccc tat caa att gat atc   528
Val Phe Glu Thr Leu Ala Leu Thr Asn Thr Pro Tyr Gln Ile Asp Ile
                165                 170                 175
cat gca ggc gga gcg gat ttg tta ttc ccc cac cat gaa aat gaa gcg   576
His Ala Gly Gly Ala Asp Leu Leu Phe Pro His His Glu Asn Glu Ala
            180                 185                 190
tgc caa acc cgt tgc gcc ttt ggc gtg gag ctt gcc aaa tat tgg atg   624
Cys Gln Thr Arg Cys Ala Phe Gly Val Glu Leu Ala Lys Tyr Trp Met
        195                 200                 205
cat aac ggc ttt gtg aat atc aat aac gaa aaa atg tct aaa agt ttg   672
His Asn Gly Phe Val Asn Ile Asn Asn Glu Lys Met Ser Lys Ser Leu
    210                 215                 220
ggg aat agc ttt ttt gtt aaa gac gct ctc aaa aac tat gat ggc gaa   720
Gly Asn Ser Phe Phe Val Lys Asp Ala Leu Lys Asn Tyr Asp Gly Glu
225                 230                 235                 240
att ttg cgc aat tac tta cta ggg gtg cat tat cgc tct gtt ttg aat   768
Ile Leu Arg Asn Tyr Leu Leu Gly Val His Tyr Arg Ser Val Leu Asn
                245                 250                 255
ttc aat gaa gaa gac ttg tta gtg agt aaa aaa cgc ttg gat aaa atc   816
Phe Asn Glu Glu Asp Leu Leu Val Ser Lys Lys Arg Leu Asp Lys Ile
            260                 265                 270
tat cgt tta aaa cag cgc gtt tta ggg act ctt gga gga ata aat cca   864
Tyr Arg Leu Lys Gln Arg Val Leu Gly Thr Leu Gly Gly Ile Asn Pro
        275                 280                 285
aac ttt aaa aaa gaa att tta gag tgc atg caa gat gat tta aac gtt   912
Asn Phe Lys Lys Glu Ile Leu Glu Cys Met Gln Asp Asp Leu Asn Val
    290                 295                 300
tct aaa gcg ttg agc gtt tta gaa agc atg ctt tct tcc act aat gaa   960
Ser Lys Ala Leu Ser Val Leu Glu Ser Met Leu Ser Ser Thr Asn Glu
305                 310                 315                 320
aaa ttg gat caa aac cct aaa aac aag gct tta aag ggc gaa att tta  1008
Lys Leu Asp Gln Asn Pro Lys Asn Lys Ala Leu Lys Gly Glu Ile Leu
                325                 330                 335
gcg aat ttg aaa ttc ata gaa gaa ctg ctt ggc atc ggg ttt aaa gac  1056
Ala Asn Leu Lys Phe Ile Glu Glu Leu Leu Gly Ile Gly Phe Lys Asp
            340                 345                 350
cct agc gcc tat ttc caa tta ggc gtg agt gaa agc gaa aaa caa gaa  1104
Pro Ser Ala Tyr Phe Gln Leu Gly Val Ser Glu Ser Glu Lys Gln Glu
        355                 360                 365
att gaa aac aag a                                               1117
Ile Glu Asn Lys
    370
<210> 176
<211> 372
<212> PRT
<213> Helicobacter pylori
<400> 176
Arg Thr Leu Glu Leu Ser Gly Tyr Glu Val Met Leu Val Arg Asn Phe
  1               5                  10                  15
Thr Asp Ile Asp Asp Lys Ile Ile Asn Lys Ala Leu Lys Glu Asn Lys
             20                  25                  30
Ser Ile Gln Glu Leu Ser Ser Ile Tyr Ile Glu Ser Tyr Thr Arg Asp
         35                  40                  45
Leu Asn Ala Leu Asn Val Lys Lys Pro Ser Leu Glu Pro Lys Ala Ser
     50                  55                  60
Glu Tyr Leu Asp Ala Met Val Gly Met Ile Glu Thr Leu Leu Glu Lys
 65                  70                  75                  80
Asn Ile Ala Tyr Gln Val Ser Asn Gly Asp Ile Tyr Leu Asp Thr Ser
                 85                  90                  95
Lys Asp Lys Asp Tyr Gly Ser Leu Ser Val His Asn Ser Ser Ile Glu
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```
                100                 105                 110
Phe Gly Arg Ile Gly Leu Val Gln Glu Lys Arg Leu Glu Gln Asp Phe
        115                 120                 125
Val Leu Trp Lys Ser Tyr Lys Gly Asp Asn Asp Val Gly Phe Asp Ser
    130                 135                 140
Pro Leu Gly Lys Gly Arg Pro Gly Trp His Ile Glu Cys Ser Ser Met
145                 150                 155                 160
Val Phe Glu Thr Leu Ala Leu Thr Asn Thr Pro Tyr Gln Ile Asp Ile
                165                 170                 175
His Ala Gly Gly Ala Asp Leu Leu Phe Pro His His Glu Asn Glu Ala
            180                 185                 190
Cys Gln Thr Arg Cys Ala Phe Gly Val Glu Leu Ala Lys Tyr Trp Met
        195                 200                 205
His Asn Gly Phe Val Asn Ile Asn Asn Glu Lys Met Ser Lys Ser Leu
    210                 215                 220
Gly Asn Ser Phe Phe Val Lys Asp Ala Leu Lys Asn Tyr Asp Gly Glu
225                 230                 235                 240
Ile Leu Arg Asn Tyr Leu Leu Gly Val His Tyr Arg Ser Val Leu Asn
                245                 250                 255
Phe Asn Glu Glu Asp Leu Leu Val Ser Lys Lys Arg Leu Asp Lys Ile
            260                 265                 270
Tyr Arg Leu Lys Gln Arg Val Leu Gly Thr Leu Gly Gly Ile Asn Pro
        275                 280                 285
Asn Phe Lys Lys Glu Ile Leu Glu Cys Met Gln Asp Asp Leu Asn Val
    290                 295                 300
Ser Lys Ala Leu Ser Val Leu Glu Ser Met Leu Ser Ser Thr Asn Glu
305                 310                 315                 320
Lys Leu Asp Gln Asn Pro Lys Asn Lys Ala Leu Lys Gly Glu Ile Leu
                325                 330                 335
Ala Asn Leu Lys Phe Ile Glu Glu Leu Leu Gly Ile Gly Phe Lys Asp
            340                 345                 350
Pro Ser Ala Tyr Phe Gln Leu Gly Val Ser Glu Ser Glu Lys Gln Glu
        355                 360                 365
Ile Glu Asn Lys
    370
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<212> DNA
<213> Helicobacter pylori
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<221> CDS
<222> (1)..(672)
<400> 177
gag gct aat aag caa gac gct tta ttg caa gct tta aaa gat gaa gcc   48
Glu Ala Asn Lys Gln Asp Ala Leu Leu Gln Ala Leu Lys Asp Glu Ala
  1               5                  10                  15
aac cat aaa aaa gaa aga gaa aaa aga gaa gtt aaa caa gaa gaa gaa   96
Asn His Lys Lys Glu Arg Glu Lys Arg Glu Val Lys Gln Glu Glu Glu
             20                  25                  30
att aaa gac atc aat ctg caa tta agc aaa atc aga gac agc ctg aaa   144
Ile Lys Asp Ile Asn Leu Gln Leu Ser Lys Ile Arg Asp Ser Leu Lys
         35                  40                  45
ctc att caa aac atg ttt tgg gat gag aaa aac ccc aat tct att aat   192
Leu Ile Gln Asn Met Phe Trp Asp Glu Lys Asn Pro Asn Ser Ile Asn
     50                  55                  60
atc cct caa gaa ttt gca gaa att tac aaa ctg gcc aaa caa agt ggg   240
Ile Pro Gln Glu Phe Ala Glu Ile Tyr Lys Leu Ala Lys Gln Ser Gly
 65                  70                  75                  80
atg aaa ccc agc cat tta gat gaa atc atg caa ttg agc ctg gaa ttg   288
Met Lys Pro Ser His Leu Asp Glu Ile Met Gln Leu Ser Leu Glu Leu
                 85                  90                  95
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atg cct tta cgc atg cgc gaa aat tcc gta acg att aag cgt tat ttt   336
Met Pro Leu Arg Met Arg Glu Asn Ser Val Thr Ile Lys Arg Tyr Phe
            100                 105                 110
aga gaa gtg ttg cgc aaa atg atc ttg tgt tgc cct gaa gat ttg aat   384
Arg Glu Val Leu Arg Lys Met Ile Leu Cys Cys Pro Glu Asp Leu Asn
        115                 120                 125
tta agg caa aaa cgc atc tta atg ctt gta ggg cca aca ggc gtg ggg   432
Leu Arg Gln Lys Arg Ile Leu Met Leu Val Gly Pro Thr Gly Val Gly
    130                 135                 140
aaa acg acg act tta gct aaa tta gcc gcg cgc tat tct agg atg tta   480
Lys Thr Thr Thr Leu Ala Lys Leu Ala Ala Arg Tyr Ser Arg Met Leu
145                 150                 155                 160
gct aaa aaa tac aag gtg ggc att atc act tta gac aat tat cgc att   528
Ala Lys Lys Tyr Lys Val Gly Ile Ile Thr Leu Asp Asn Tyr Arg Ile
                165                 170                 175
ggg gct ttg gag caa tta agc tgg tat gct aat aaa atg aaa atg agt   576
Gly Ala Leu Glu Gln Leu Ser Trp Tyr Ala Asn Lys Met Lys Met Ser
            180                 185                 190
ata gaa gcg gtg att gac gct aag gat ttt gct aaa gaa att gaa gcg   624
Ile Glu Ala Val Ile Asp Ala Lys Asp Phe Ala Lys Glu Ile Glu Ala
        195                 200                 205
ttg gaa tac tgc gat ttt att tta gtg gat acg aca ggg cat tcg caa t 673
Leu Glu Tyr Cys Asp Phe Ile Leu Val Asp Thr Thr Gly His Ser Gln
    210                 215                 220
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<211> 224
<212> PRT
<213> Helicobacter pylori
<400> 178
Glu Ala Asn Lys Gln Asp Ala Leu Leu Gln Ala Leu Lys Asp Glu Ala
  1               5                  10                  15
Asn His Lys Lys Glu Arg Glu Lys Arg Glu Val Lys Gln Glu Glu Glu
             20                  25                  30
Ile Lys Asp Ile Asn Leu Gln Leu Ser Lys Ile Arg Asp Ser Leu Lys
         35                  40                  45
Leu Ile Gln Asn Met Phe Trp Asp Glu Lys Asn Pro Asn Ser Ile Asn
     50                  55                  60
Ile Pro Gln Glu Phe Ala Glu Ile Tyr Lys Leu Ala Lys Gln Ser Gly
 65                  70                  75                  80
Met Lys Pro Ser His Leu Asp Glu Ile Met Gln Leu Ser Leu Glu Leu
                 85                  90                  95
Met Pro Leu Arg Met Arg Glu Asn Ser Val Thr Ile Lys Arg Tyr Phe
            100                 105                 110
Arg Glu Val Leu Arg Lys Met Ile Leu Cys Cys Pro Glu Asp Leu Asn
        115                 120                 125
Leu Arg Gln Lys Arg Ile Leu Met Leu Val Gly Pro Thr Gly Val Gly
    130                 135                 140
Lys Thr Thr Thr Leu Ala Lys Leu Ala Ala Arg Tyr Ser Arg Met Leu
145                 150                 155                 160
Ala Lys Lys Tyr Lys Val Gly Ile Ile Thr Leu Asp Asn Tyr Arg Ile
                165                 170                 175
Gly Ala Leu Glu Gln Leu Ser Trp Tyr Ala Asn Lys Met Lys Met Ser
            180                 185                 190
Ile Glu Ala Val Ile Asp Ala Lys Asp Phe Ala Lys Glu Ile Glu Ala
        195                 200                 205
Leu Glu Tyr Cys Asp Phe Ile Leu Val Asp Thr Thr Gly His Ser Gln
    210                 215                 220
<210> 179
<211> 43
<212> DNA
<213> Helicobacter pylori
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<220>
<221> CDS
<222> (1)..(42)
<400> 179
gac tat aaa gat tta gac atg ctc aag cac acg cta tca gag c 43
Asp Tyr Lys Asp Leu Asp Met Leu Lys His Thr Leu Ser Glu
1 5 10
<210> 180
<211> 14
<212> PRT
<213> Helicobacter pylori
<400> 180
Asp Tyr Lys Asp Leu Asp Met Leu Lys His Thr Leu Ser Glu
1 5 10
<210> 181
<211> 238
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(237)
<400> 181
gag cgc cta gaa aaa gaa att gaa gtc att acg aac atg aaa ttc cca 48
Glu Arg Leu Glu Lys Glu Ile Glu Val Ile Thr Asn Met Lys Phe Pro
1 5 10 15
ggg tat atg ctg att gtg tgg gat ttt atc cgt tat gct aag gaa atg 96
Gly Tyr Met Leu Ile Val Trp Asp Phe Ile Arg Tyr Ala Lys Glu Met
20 25 30
ggc att cct gta ggg cct ggt agg ggg agt gcg gcc ggg agc ttg gtg 144
Gly Ile Pro Val Gly Pro Gly Arg Gly Ser Ala Ala Gly Ser Leu Val
35 40 45
gct ttt gct tta aaa atc acg gat att gac cct ttg aaa tac gat ttg 192
Ala Phe Ala Leu Lys Ile Thr Asp Ile Asp Pro Leu Lys Tyr Asp Leu
50 55 60
ctc ttt gaa agg ttt tta aac ccc gaa aga atc agc atg cct gat a 238
Leu Phe Glu Arg Phe Leu Asn Pro Glu Arg Ile Ser Met Pro Asp
65 70 75
<210> 182
<211> 79
<212> PRT
<213> Helicobacter pylori
<400> 182
Glu Arg Leu Glu Lys Glu Ile Glu Val Ile Thr Asn Met Lys Phe Pro
1 5 10 15
Gly Tyr Met Leu Ile Val Trp Asp Phe Ile Arg Tyr Ala Lys Glu Met
20 25 30
Gly Ile Pro Val Gly Pro Gly Arg Gly Ser Ala Ala Gly Ser Leu Val
35 40 45
Ala Phe Ala Leu Lys Ile Thr Asp Ile Asp Pro Leu Lys Tyr Asp Leu
50 55 60
Leu Phe Glu Arg Phe Leu Asn Pro Glu Arg Ile Ser Met Pro Asp
65 70 75
<210> 183
<211> 1588
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(1587)
<400> 183
aat tta ggg aat gca aac aac acc att tac tat tac gac aag agc att 48

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Asn Leu Gly Asn Ala Asn Asn Thr Ile Tyr Tyr Tyr Asp Lys Ser Ile
 1               5                  10                  15
gat ttt tat gcg agc ggg aaa act cta ttc act aaa gcg gaa ttt tct   96
Asp Phe Tyr Ala Ser Gly Lys Thr Leu Phe Thr Lys Ala Glu Phe Ser
            20                  25                  30
caa aca ttc acc ggg caa aac agc gcg atc gtt ttt ggg gct aaa agc   144
Gln Thr Phe Thr Gly Gln Asn Ser Ala Ile Val Phe Gly Ala Lys Ser
        35                  40                  45
ata tgg acg agc tta agc gat gca ccg cag tct aac acc atc att cgc   192
Ile Trp Thr Ser Leu Ser Asp Ala Pro Gln Ser Asn Thr Ile Ile Arg
    50                  55                  60
ttt ggg gac aat aag gga gca ggg agt aat gat gcg agc ggg cat tgc   240
Phe Gly Asp Asn Lys Gly Ala Gly Ser Asn Asp Ala Ser Gly His Cys
65                  70                  75                  80
tgg aat ttg caa tgc ata ggc ttt att aca ggg cat tat gaa gcg caa   288
Trp Asn Leu Gln Cys Ile Gly Phe Ile Thr Gly His Tyr Glu Ala Gln
                85                  90                  95
aag att tac atc acc ggt agc att gaa agc ggg aat cgc att tct agc   336
Lys Ile Tyr Ile Thr Gly Ser Ile Glu Ser Gly Asn Arg Ile Ser Ser
            100                 105                 110
ggt ggg ggc gcg agc ctt aat ttt aac ggg ctt caa ggc att ctt tta   384
Gly Gly Gly Ala Ser Leu Asn Phe Asn Gly Leu Gln Gly Ile Leu Leu
        115                 120                 125
acg aac gcg act ttg tat aac cgc gcc gct ggc acg caa agc tcg tct   432
Thr Asn Ala Thr Leu Tyr Asn Arg Ala Ala Gly Thr Gln Ser Ser Ser
    130                 135                 140
atg aat ttt atc tct aac agc gcg aac att cag gct caa aac tcc tat   480
Met Asn Phe Ile Ser Asn Ser Ala Asn Ile Gln Ala Gln Asn Ser Tyr
145                 150                 155                 160
ttt ata gac gat acc gca caa aat ggc ggt aac cct aat ttc agt ttc   528
Phe Ile Asp Asp Thr Ala Gln Asn Gly Gly Asn Pro Asn Phe Ser Phe
                165                 170                 175
aac gct ttg aat ctg gat ttt tct aac agc tct ttt aga ggc tat gtg   576
Asn Ala Leu Asn Leu Asp Phe Ser Asn Ser Ser Phe Arg Gly Tyr Val
            180                 185                 190
ggg aaa acg caa tct gtt ttt aaa ttc aat gcc aag aat gcg atc agt   624
Gly Lys Thr Gln Ser Val Phe Lys Phe Asn Ala Lys Asn Ala Ile Ser
        195                 200                 205
ttc acc aac agc acg aat tta agc tct ggt ttg tat caa atg caa gct   672
Phe Thr Asn Ser Thr Asn Leu Ser Ser Gly Leu Tyr Gln Met Gln Ala
    210                 215                 220
aaa agc gtg ttg ttt gac aat tcc aat tta agc gtt tca gtg ggg aca   720
Lys Ser Val Leu Phe Asp Asn Ser Asn Leu Ser Val Ser Val Gly Thr
225                 230                 235                 240
agc agt att aaa gcc aat gcg atc aat ctt tct caa aat gcc tct att   768
Ser Ser Ile Lys Ala Asn Ala Ile Asn Leu Ser Gln Asn Ala Ser Ile
                245                 250                 255
aat gcg agc aac cat tca acc tta gaa ctt caa ggc gat ttg aat gtg   816
Asn Ala Ser Asn His Ser Thr Leu Glu Leu Gln Gly Asp Leu Asn Val
            260                 265                 270
aac gac acc agc tcg ctc aac ctc aac caa agc acg att aat gtt tcc   864
Asn Asp Thr Ser Ser Leu Asn Leu Asn Gln Ser Thr Ile Asn Val Ser
        275                 280                 285
aat aac gcc acg atc aac gat tat gcg agc ttg att gcg agt aat ggc   912
Asn Asn Ala Thr Ile Asn Asp Tyr Ala Ser Leu Ile Ala Ser Asn Gly
    290                 295                 300
tct cac ctt aat ttt aac ggg gcg gtt aat ttc aat tca gcg aat att   960
Ser His Leu Asn Phe Asn Gly Ala Val Asn Phe Asn Ser Ala Asn Ile
305                 310                 315                 320
act acg agt ttg aat aat tcc tct atc gtg ttt aag ggg gcg gtc tct   1008
Thr Thr Ser Leu Asn Asn Ser Ser Ile Val Phe Lys Gly Ala Val Ser
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                325                 330                 335
tta gga ggg cag ttt aat tta agc aat aac tct tct tta gat ttc caa   1056
Leu Gly Gly Gln Phe Asn Leu Ser Asn Asn Ser Ser Leu Asp Phe Gln
            340                 345                 350
ggc tct agc gct atc acc tct aac acg gcg ttt aat ttc tat gat aac   1104
Gly Ser Ser Ala Ile Thr Ser Asn Thr Ala Phe Asn Phe Tyr Asp Asn
        355                 360                 365
gct ttt tct caa agc ccc atc act ttc cat caa gcc ctt gac att aaa   1152
Ala Phe Ser Gln Ser Pro Ile Thr Phe His Gln Ala Leu Asp Ile Lys
    370                 375                 380
gcg ccc tta agt ttg gga ggc aac ctt tta aac cct aac aac agc agc   1200
Ala Pro Leu Ser Leu Gly Gly Asn Leu Leu Asn Pro Asn Asn Ser Ser
385                 390                 395                 400
gtg ctg gat tta aaa aac agc cag ctt gtt ttt ggc gat caa ggg agt   1248
Val Leu Asp Leu Lys Asn Ser Gln Leu Val Phe Gly Asp Gln Gly Ser
                405                 410                 415
ttg aat atc gct aac att gat tta cta agc gat cta aat gat aat aaa   1296
Leu Asn Ile Ala Asn Ile Asp Leu Leu Ser Asp Leu Asn Asp Asn Lys
            420                 425                 430
aat cgt gtg tat aac atc att caa gcg gac atg aat agt aat tgg tat   1344
Asn Arg Val Tyr Asn Ile Ile Gln Ala Asp Met Asn Ser Asn Trp Tyr
        435                 440                 445
gag cgt atc agc ttc ttt ggc atg cac atc aat gac ggg att tat gat   1392
Glu Arg Ile Ser Phe Phe Gly Met His Ile Asn Asp Gly Ile Tyr Asp
    450                 455                 460
gct aaa aac caa act tat agt ttc act aac ccc ctt aat aac gcc cta   1440
Ala Lys Asn Gln Thr Tyr Ser Phe Thr Asn Pro Leu Asn Asn Ala Leu
465                 470                 475                 480
aaa atc acc gag agc ttt aaa gac aac caa cta agc gtt acg ctc tct   1488
Lys Ile Thr Glu Ser Phe Lys Asp Asn Gln Leu Ser Val Thr Leu Ser
                485                 490                 495
caa atc ccg ggt att aaa aac acg ctc tat aac att ggc tct gaa att   1536
Gln Ile Pro Gly Ile Lys Asn Thr Leu Tyr Asn Ile Gly Ser Glu Ile
            500                 505                 510
ttt aac tac caa aaa gtt tat aac aac gct aat ggc gtg tat tct tat   1584
Phe Asn Tyr Gln Lys Val Tyr Asn Asn Ala Asn Gly Val Tyr Ser Tyr
        515                 520                 525
agc g                                                            1588
Ser
<210> 184
<211> 529
<212> PRT
<213> Helicobacter pylori
<400> 184
Asn Leu Gly Asn Ala Asn Asn Thr Ile Tyr Tyr Tyr Asp Lys Ser Ile
  1               5                  10                  15
Asp Phe Tyr Ala Ser Gly Lys Thr Leu Phe Thr Lys Ala Glu Phe Ser
             20                  25                  30
Gln Thr Phe Thr Gly Gln Asn Ser Ala Ile Val Phe Gly Ala Lys Ser
         35                  40                  45
Ile Trp Thr Ser Leu Ser Asp Ala Pro Gln Ser Asn Thr Ile Ile Arg
     50                  55                  60
Phe Gly Asp Asn Lys Gly Ala Gly Ser Asn Asp Ala Ser Gly His Cys
 65                  70                  75                  80
Trp Asn Leu Gln Cys Ile Gly Phe Ile Thr Gly His Tyr Glu Ala Gln
                 85                  90                  95
Lys Ile Tyr Ile Thr Gly Ser Ile Glu Ser Gly Asn Arg Ile Ser Ser
            100                 105                 110
Gly Gly Gly Ala Ser Leu Asn Phe Asn Gly Leu Gln Gly Ile Leu Leu
        115                 120                 125
Thr Asn Ala Thr Leu Tyr Asn Arg Ala Ala Gly Thr Gln Ser Ser Ser
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    130                 135                 140
Met Asn Phe Ile Ser Asn Ser Ala Asn Ile Gln Ala Gln Asn Ser Tyr
145                 150                 155                 160
Phe Ile Asp Asp Thr Ala Gln Asn Gly Gly Asn Pro Asn Phe Ser Phe
                165                 170                 175
Asn Ala Leu Asn Leu Asp Phe Ser Asn Ser Ser Phe Arg Gly Tyr Val
            180                 185                 190
Gly Lys Thr Gln Ser Val Phe Lys Phe Asn Ala Lys Asn Ala Ile Ser
        195                 200                 205
Phe Thr Asn Ser Thr Asn Leu Ser Ser Gly Leu Tyr Gln Met Gln Ala
    210                 215                 220
Lys Ser Val Leu Phe Asp Asn Ser Asn Leu Ser Val Ser Val Gly Thr
225                 230                 235                 240
Ser Ser Ile Lys Ala Asn Ala Ile Asn Leu Ser Gln Asn Ala Ser Ile
                245                 250                 255
Asn Ala Ser Asn His Ser Thr Leu Glu Leu Gln Gly Asp Leu Asn Val
            260                 265                 270
Asn Asp Thr Ser Ser Leu Asn Leu Asn Gln Ser Thr Ile Asn Val Ser
        275                 280                 285
Asn Asn Ala Thr Ile Asn Asp Tyr Ala Ser Leu Ile Ala Ser Asn Gly
    290                 295                 300
Ser His Leu Asn Phe Asn Gly Ala Val Asn Phe Asn Ser Ala Asn Ile
305                 310                 315                 320
Thr Thr Ser Leu Asn Asn Ser Ser Ile Val Phe Lys Gly Ala Val Ser
                325                 330                 335
Leu Gly Gly Gln Phe Asn Leu Ser Asn Asn Ser Ser Leu Asp Phe Gln
            340                 345                 350
Gly Ser Ser Ala Ile Thr Ser Asn Thr Ala Phe Asn Phe Tyr Asp Asn
        355                 360                 365
Ala Phe Ser Gln Ser Pro Ile Thr Phe His Gln Ala Leu Asp Ile Lys
    370                 375                 380
Ala Pro Leu Ser Leu Gly Gly Asn Leu Leu Asn Pro Asn Asn Ser Ser
385                 390                 395                 400
Val Leu Asp Leu Lys Asn Ser Gln Leu Val Phe Gly Asp Gln Gly Ser
                405                 410                 415
Leu Asn Ile Ala Asn Ile Asp Leu Leu Ser Asp Leu Asn Asp Asn Lys
            420                 425                 430
Asn Arg Val Tyr Asn Ile Ile Gln Ala Asp Met Asn Ser Asn Trp Tyr
        435                 440                 445
Glu Arg Ile Ser Phe Phe Gly Met His Ile Asn Asp Gly Ile Tyr Asp
    450                 455                 460
Ala Lys Asn Gln Thr Tyr Ser Phe Thr Asn Pro Leu Asn Asn Ala Leu
465                 470                 475                 480
Lys Ile Thr Glu Ser Phe Lys Asp Asn Gln Leu Ser Val Thr Leu Ser
                485                 490                 495
Gln Ile Pro Gly Ile Lys Asn Thr Leu Tyr Asn Ile Gly Ser Glu Ile
            500                 505                 510
Phe Asn Tyr Gln Lys Val Tyr Asn Asn Ala Asn Gly Val Tyr Ser Tyr
        515                 520                 525
Ser
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<210> 185
<211> 1735
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(1734)
<400> 185

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gct gat cgc acc acg aga gtg gat ttc aac gct aaa aat atc tta att   48
Ala Asp Arg Thr Thr Arg Val Asp Phe Asn Ala Lys Asn Ile Leu Ile
```

```
 1               5                  10                  15
gat aat ttt tta gaa atc aat aat cgt gtg ggt tct gga gcc ggg agg   96
Asp Asn Phe Leu Glu Ile Asn Asn Arg Val Gly Ser Gly Ala Gly Arg
            20                  25                  30
aaa gcc agc tct acg gtt tta act ttg caa gct tca gaa ggg att act  144
Lys Ala Ser Ser Thr Val Leu Thr Leu Gln Ala Ser Glu Gly Ile Thr
        35                  40                  45
agc agt aaa aat gcg gaa att tct ctt tat gat ggc gcc acg ctc aat  192
Ser Ser Lys Asn Ala Glu Ile Ser Leu Tyr Asp Gly Ala Thr Leu Asn
    50                  55                  60
ttg gct tca aac agc gtt aaa tta atg ggt aat gtg tgg atg ggc cgt  240
Leu Ala Ser Asn Ser Val Lys Leu Met Gly Asn Val Trp Met Gly Arg
65                  70                  75                  80
ttg caa tat gtg gga gcg tat ttg gcc cct tca tac agc acg ata aac  288
Leu Gln Tyr Val Gly Ala Tyr Leu Ala Pro Ser Tyr Ser Thr Ile Asn
                85                  90                  95
act tca aaa gtg aca ggg gaa gtg aat ttt aac cat ctc act gtg ggc  336
Thr Ser Lys Val Thr Gly Glu Val Asn Phe Asn His Leu Thr Val Gly
            100                 105                 110
gat cac aac gcc gct caa gca ggc att atc gct agt aac aag act cat  384
Asp His Asn Ala Ala Gln Ala Gly Ile Ile Ala Ser Asn Lys Thr His
        115                 120                 125
att ggc aca ctg gat ttg tgg caa agc gcg gga cta aac att atc gcc  432
Ile Gly Thr Leu Asp Leu Trp Gln Ser Ala Gly Leu Asn Ile Ile Ala
    130                 135                 140
cct cca gaa ggc ggt tat aag gat aaa cct aag gat aaa cct agt aac  480
Pro Pro Glu Gly Gly Tyr Lys Asp Lys Pro Lys Asp Lys Pro Ser Asn
145                 150                 155                 160
acc acg caa aat aat gct aac aac aac caa caa aac agc gct caa aac  528
Thr Thr Gln Asn Asn Ala Asn Asn Asn Gln Gln Asn Ser Ala Gln Asn
                165                 170                 175
aat agt aac act cag gtt att aac cca ccc aat agc gcg caa aaa aca  576
Asn Ser Asn Thr Gln Val Ile Asn Pro Pro Asn Ser Ala Gln Lys Thr
            180                 185                 190
gaa att caa ccc acg caa gtc att gat ggg cct ttt gct ggt ggc aaa  624
Glu Ile Gln Pro Thr Gln Val Ile Asp Gly Pro Phe Ala Gly Gly Lys
        195                 200                 205
gac acg gtt gtc aat att gat cgc atc aac act aac gct gat ggc acg  672
Asp Thr Val Val Asn Ile Asp Arg Ile Asn Thr Asn Ala Asp Gly Thr
    210                 215                 220
att aaa gtg gga ggg tat aaa gct tct ctt acc acc aat gcg gct cat  720
Ile Lys Val Gly Gly Tyr Lys Ala Ser Leu Thr Thr Asn Ala Ala His
225                 230                 235                 240
ttg cat atc ggc aaa ggc ggt atc aat ctg tcc aat caa gcg agc ggg  768
Leu His Ile Gly Lys Gly Gly Ile Asn Leu Ser Asn Gln Ala Ser Gly
                245                 250                 255
cgc acc ctt tta gtg gaa aat cta acc ggg aat atc acc gtt gat ggg  816
Arg Thr Leu Leu Val Glu Asn Leu Thr Gly Asn Ile Thr Val Asp Gly
            260                 265                 270
cct tta aga gtg aat aat caa gtg ggt ggt tat gct ttg gca gga tca  864
Pro Leu Arg Val Asn Asn Gln Val Gly Gly Tyr Ala Leu Ala Gly Ser
        275                 280                 285
agc gcg aat ttt gag ttt aag gct ggt acg gat acc aaa aac ggc aca  912
Ser Ala Asn Phe Glu Phe Lys Ala Gly Thr Asp Thr Lys Asn Gly Thr
    290                 295                 300
gcc act ttt aat aac gat att agt ttg gga aga ttt gtg aat tta aaa  960
Ala Thr Phe Asn Asn Asp Ile Ser Leu Gly Arg Phe Val Asn Leu Lys
305                 310                 315                 320
gtg gat gct cat aca gct aat ttt aaa ggt att gat act ggt aat ggt 1008
Val Asp Ala His Thr Ala Asn Phe Lys Gly Ile Asp Thr Gly Asn Gly
                325                 330                 335
```

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ggt ttc aac acc tta gat ttt agt ggc gtt aca ggt aag gtc aat atc   1056
Gly Phe Asn Thr Leu Asp Phe Ser Gly Val Thr Gly Lys Val Asn Ile
            340                 345                 350
aac aag ctc att acg gct tcc act aat gtg gcc gtt aaa aac ttc aac   1104
Asn Lys Leu Ile Thr Ala Ser Thr Asn Val Ala Val Lys Asn Phe Asn
        355                 360                 365
att aat gaa ttg gtt gtt aag acc aat ggg gtg agt gtg ggg gaa tac   1152
Ile Asn Glu Leu Val Val Lys Thr Asn Gly Val Ser Val Gly Glu Tyr
    370                 375                 380
act cat ttt agc gaa gat ata ggc agt caa tcg cgc atc aat acc gtg   1200
Thr His Phe Ser Glu Asp Ile Gly Ser Gln Ser Arg Ile Asn Thr Val
385                 390                 395                 400
cgt ttg gaa act ggc act agg tca atc ttt tct ggg ggt gtc aaa ttt   1248
Arg Leu Glu Thr Gly Thr Arg Ser Ile Phe Ser Gly Gly Val Lys Phe
                405                 410                 415
aaa agc ggt gaa aaa ctg gtt ata gat gag ttt tac tat agc cct tgg   1296
Lys Ser Gly Glu Lys Leu Val Ile Asp Glu Phe Tyr Tyr Ser Pro Trp
            420                 425                 430
aat tat ttt gac gct agg aat att aaa aat gtt gaa atc acc aga aaa   1344
Asn Tyr Phe Asp Ala Arg Asn Ile Lys Asn Val Glu Ile Thr Arg Lys
        435                 440                 445
ttc gct tct tca acc cca gaa aac cct tgg ggc aca tca aag ctt atg   1392
Phe Ala Ser Ser Thr Pro Glu Asn Pro Trp Gly Thr Ser Lys Leu Met
    450                 455                 460
ttt aat aat cta acc ctg ggt caa aat gcg gtc atg gac tat agt caa   1440
Phe Asn Asn Leu Thr Leu Gly Gln Asn Ala Val Met Asp Tyr Ser Gln
465                 470                 475                 480
ttt tca aat tta acc att cag ggg gat ttc atc aac aat caa ggc act   1488
Phe Ser Asn Leu Thr Ile Gln Gly Asp Phe Ile Asn Asn Gln Gly Thr
                485                 490                 495
atc aat tat ttg gtc cga ggc ggg caa gta gcc acc ttg aat gta ggc   1536
Ile Asn Tyr Leu Val Arg Gly Gly Gln Val Ala Thr Leu Asn Val Gly
            500                 505                 510
aat gcg gca gct atg ttc ttt agt aat aat gtg gat agc gcg act ggg   1584
Asn Ala Ala Ala Met Phe Phe Ser Asn Asn Val Asp Ser Ala Thr Gly
        515                 520                 525
ttt tac caa ccg ctc atg aag att aac agc gct caa gat ctc att aaa   1632
Phe Tyr Gln Pro Leu Met Lys Ile Asn Ser Ala Gln Asp Leu Ile Lys
    530                 535                 540
aat aaa gaa cat gtc tta ttg aaa gcg aaa atc atc ggt tat ggc aat   1680
Asn Lys Glu His Val Leu Leu Lys Ala Lys Ile Ile Gly Tyr Gly Asn
545                 550                 555                 560
gtt tct tta ggc act aac agc att agt aat gtt aat cta ata gag caa   1728
Val Ser Leu Gly Thr Asn Ser Ile Ser Asn Val Asn Leu Ile Glu Gln
                565                 570                 575
ttc aaa g                                                        1735
Phe Lys
<210> 186
<211> 578
<212> PRT
<213> Helicobacter pylori
<400> 186
Ala Asp Arg Thr Thr Arg Val Asp Phe Asn Ala Lys Asn Ile Leu Ile
  1               5                  10                  15
Asp Asn Phe Leu Glu Ile Asn Asn Arg Val Gly Ser Gly Ala Gly Arg
             20                  25                  30
Lys Ala Ser Ser Thr Val Leu Thr Leu Gln Ala Ser Glu Gly Ile Thr
         35                  40                  45
Ser Ser Lys Asn Ala Glu Ile Ser Leu Tyr Asp Gly Ala Thr Leu Asn
     50                  55                  60
Leu Ala Ser Asn Ser Val Lys Leu Met Gly Asn Val Trp Met Gly Arg
```

65 70 75 80
Leu Gln Tyr Val Gly Ala Tyr Leu Ala Pro Ser Tyr Ser Thr Ile Asn
85 90 95
Thr Ser Lys Val Thr Gly Glu Val Asn Phe Asn His Leu Thr Val Gly
100 105 110
Asp His Asn Ala Ala Gln Ala Gly Ile Ile Ala Ser Asn Lys Thr His
115 120 125
Ile Gly Thr Leu Asp Leu Trp Gln Ser Ala Gly Leu Asn Ile Ile Ala
130 135 140
Pro Pro Glu Gly Gly Tyr Lys Asp Lys Pro Lys Asp Lys Pro Ser Asn
145 150 155 160
Thr Thr Gln Asn Asn Ala Asn Asn Asn Gln Gln Asn Ser Ala Gln Asn
165 170 175
Asn Ser Asn Thr Gln Val Ile Asn Pro Pro Asn Ser Ala Gln Lys Thr
180 185 190
Glu Ile Gln Pro Thr Gln Val Ile Asp Gly Pro Phe Ala Gly Gly Lys
195 200 205
Asp Thr Val Val Asn Ile Asp Arg Ile Asn Thr Asn Ala Asp Gly Thr
210 215 220
Ile Lys Val Gly Gly Tyr Lys Ala Ser Leu Thr Thr Asn Ala Ala His
225 230 235 240
Leu His Ile Gly Lys Gly Gly Ile Asn Leu Ser Asn Gln Ala Ser Gly
245 250 255
Arg Thr Leu Leu Val Glu Asn Leu Thr Gly Asn Ile Thr Val Asp Gly
260 265 270
Pro Leu Arg Val Asn Asn Gln Val Gly Gly Tyr Ala Leu Ala Gly Ser
275 280 285
Ser Ala Asn Phe Glu Phe Lys Ala Gly Thr Asp Thr Lys Asn Gly Thr
290 295 300
Ala Thr Phe Asn Asn Asp Ile Ser Leu Gly Arg Phe Val Asn Leu Lys
305 310 315 320
Val Asp Ala His Thr Ala Asn Phe Lys Gly Ile Asp Thr Gly Asn Gly
325 330 335
Gly Phe Asn Thr Leu Asp Phe Ser Gly Val Thr Gly Lys Val Asn Ile
340 345 350
Asn Lys Leu Ile Thr Ala Ser Thr Asn Val Ala Val Lys Asn Phe Asn
355 360 365
Ile Asn Glu Leu Val Val Lys Thr Asn Gly Val Ser Val Gly Glu Tyr
370 375 380
Thr His Phe Ser Glu Asp Ile Gly Ser Gln Ser Arg Ile Asn Thr Val
385 390 395 400
Arg Leu Glu Thr Gly Thr Arg Ser Ile Phe Ser Gly Gly Val Lys Phe
405 410 415
Lys Ser Gly Glu Lys Leu Val Ile Asp Glu Phe Tyr Tyr Ser Pro Trp
420 425 430
Asn Tyr Phe Asp Ala Arg Asn Ile Lys Asn Val Glu Ile Thr Arg Lys
435 440 445
Phe Ala Ser Ser Thr Pro Glu Asn Pro Trp Gly Thr Ser Lys Leu Met
450 455 460
Phe Asn Asn Leu Thr Leu Gly Gln Asn Ala Val Met Asp Tyr Ser Gln
465 470 475 480
Phe Ser Asn Leu Thr Ile Gln Gly Asp Phe Ile Asn Asn Gln Gly Thr
485 490 495
Ile Asn Tyr Leu Val Arg Gly Gly Gln Val Ala Thr Leu Asn Val Gly
500 505 510
Asn Ala Ala Ala Met Phe Phe Ser Asn Asn Val Asp Ser Ala Thr Gly
515 520 525
Phe Tyr Gln Pro Leu Met Lys Ile Asn Ser Ala Gln Asp Leu Ile Lys
530 535 540
Asn Lys Glu His Val Leu Leu Lys Ala Lys Ile Ile Gly Tyr Gly Asn
545 550 555 560

```
Val Ser Leu Gly Thr Asn Ser Ile Ser Asn Val Asn Leu Ile Glu Gln
                565                 570                 575
Phe Lys

<210> 187
<211> 666
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(666)
<400> 187
agt ttt ttg gta agc ttt ttg gtt gct gaa aac gct cat gag cca gaa   48
Ser Phe Leu Val Ser Phe Leu Val Ala Glu Asn Ala His Glu Pro Glu
  1               5                  10                  15
gaa atc aag gct aaa gtg gct tat gtg aaa atc ccc caa tta gaa gat   96
Glu Ile Lys Ala Lys Val Ala Tyr Val Lys Ile Pro Gln Leu Glu Asp
            20                  25                  30
ttg gaa aac aac ccg gtt tat atc ggt caa att ata ggc gta act tat   144
Leu Glu Asn Asn Pro Val Tyr Ile Gly Gln Ile Ile Gly Val Thr Tyr
        35                  40                  45
gat tta ttg ctg ttt gac gct gag ttt ttg gaa gcc aaa atc aaa gac   192
Asp Leu Leu Leu Phe Asp Ala Glu Phe Leu Glu Ala Lys Ile Lys Asp
    50                  55                  60
ggg ttg gat aaa acc caa att gag ctt tta aac aag atg cct aaa tgg   240
Gly Leu Asp Lys Thr Gln Ile Glu Leu Leu Asn Lys Met Pro Lys Trp
65                  70                  75                  80
aaa aag gtg gaa aaa gag ctt ttc aga gcg act tat tat tac aag att   288
Lys Lys Val Glu Lys Glu Leu Phe Arg Ala Thr Tyr Tyr Tyr Lys Ile
                85                  90                  95
aag ggc ata aaa gcg att att ccg tcc tta gaa gtg agc gcg ttt tcc   336
Lys Gly Ile Lys Ala Ile Ile Pro Ser Leu Glu Val Ser Ala Phe Ser
            100                 105                 110
aat aaa gac aaa tac ata gat cat tcc ata gcc cca aaa gtt act ttg   384
Asn Lys Asp Lys Tyr Ile Asp His Ser Ile Ala Pro Lys Val Thr Leu
        115                 120                 125
cag gta acg gat ttg tcc aaa aac cct cgt tat gcg aat gtc atg gct   432
Gln Val Thr Asp Leu Ser Lys Asn Pro Arg Tyr Ala Asn Val Met Ala
    130                 135                 140
aaa gat tta caa gtc ttg caa tac aaa acc aaa gat tat gac gat aaa   480
Lys Asp Leu Gln Val Leu Gln Tyr Lys Thr Lys Asp Tyr Asp Asp Lys
145                 150                 155                 160
aac aat att ttg gtg atg gaa ata gcg ttc aaa gaa gcc act tgg gaa   528
Asn Asn Ile Leu Val Met Glu Ile Ala Phe Lys Glu Ala Thr Trp Glu
                165                 170                 175
gat ttt cac atc aaa gaa gcg atc aag caa ggg ttt gat aac gcc tct   576
Asp Phe His Ile Lys Glu Ala Ile Lys Gln Gly Phe Asp Asn Ala Ser
            180                 185                 190
tta aac cag atc aag gct aaa gaa ggg agc gtt ttt tat tat tgc gtg   624
Leu Asn Gln Ile Lys Ala Lys Glu Gly Ser Val Phe Tyr Tyr Cys Val
        195                 200                 205
ttg cct aag act att caa aac ctt tct ttt gat tat ttc tcg           666
Leu Pro Lys Thr Ile Gln Asn Leu Ser Phe Asp Tyr Phe Ser
    210                 215                 220
<210> 188
<211> 222
<212> PRT
<213> Helicobacter pylori
<400> 188
Ser Phe Leu Val Ser Phe Leu Val Ala Glu Asn Ala His Glu Pro Glu
  1               5                  10                  15
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```
Glu Ile Lys Ala Lys Val Ala Tyr Val Lys Ile Pro Gln Leu Glu Asp
            20                  25                  30
Leu Glu Asn Asn Pro Val Tyr Ile Gly Gln Ile Ile Gly Val Thr Tyr
        35                  40                  45
Asp Leu Leu Leu Phe Asp Ala Glu Phe Leu Glu Ala Lys Ile Lys Asp
    50                  55                  60
Gly Leu Asp Lys Thr Gln Ile Glu Leu Leu Asn Lys Met Pro Lys Trp
65                  70                  75                  80
Lys Lys Val Glu Lys Glu Leu Phe Arg Ala Thr Tyr Tyr Tyr Lys Ile
                85                  90                  95
Lys Gly Ile Lys Ala Ile Ile Pro Ser Leu Glu Val Ser Ala Phe Ser
            100                 105                 110
Asn Lys Asp Lys Tyr Ile Asp His Ser Ile Ala Pro Lys Val Thr Leu
        115                 120                 125
Gln Val Thr Asp Leu Ser Lys Asn Pro Arg Tyr Ala Asn Val Met Ala
    130                 135                 140
Lys Asp Leu Gln Val Leu Gln Tyr Lys Thr Lys Asp Tyr Asp Asp Lys
145                 150                 155                 160
Asn Asn Ile Leu Val Met Glu Ile Ala Phe Lys Glu Ala Thr Trp Glu
                165                 170                 175
Asp Phe His Ile Lys Glu Ala Ile Lys Gln Gly Phe Asp Asn Ala Ser
            180                 185                 190
Leu Asn Gln Ile Lys Ala Lys Glu Gly Ser Val Phe Tyr Tyr Cys Val
        195                 200                 205
Leu Pro Lys Thr Ile Gln Asn Leu Ser Phe Asp Tyr Phe Ser
    210                 215                 220
<210> 189
<211> 186
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(186)
<400> 189
gga gcc aag agc gtt cta gtc gct aat atc atg gtc gtt caa acc ccc   48
Gly Ala Lys Ser Val Leu Val Ala Asn Ile Met Val Val Gln Thr Pro
  1               5                  10                  15
att gag ctt tcc acc gtg aat tat tta gcc cct tta att ttc aat ttg   96
Ile Glu Leu Ser Thr Val Asn Tyr Leu Ala Pro Leu Ile Phe Asn Leu
            20                  25                  30
gac aag cag ctc atg ggg caa gtg gtt ttg gat tct aac aaa tac cca   144
Asp Lys Gln Leu Met Gly Gln Val Val Leu Asp Ser Asn Lys Tyr Pro
        35                  40                  45
cac tac cat tta aga gag aat att cta agc cac acg cat gaa           186
His Tyr His Leu Arg Glu Asn Ile Leu Ser His Thr His Glu
    50                  55                  60
<210> 190
<211> 62
<212> PRT
<213> Helicobacter pylori
<400> 190
Gly Ala Lys Ser Val Leu Val Ala Asn Ile Met Val Val Gln Thr Pro
  1               5                  10                  15
Ile Glu Leu Ser Thr Val Asn Tyr Leu Ala Pro Leu Ile Phe Asn Leu
            20                  25                  30
Asp Lys Gln Leu Met Gly Gln Val Val Leu Asp Ser Asn Lys Tyr Pro
        35                  40                  45
His Tyr His Leu Arg Glu Asn Ile Leu Ser His Thr His Glu
    50                  55                  60
<210> 191
<211> 864
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<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(864)
<400> 191

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gat aag gga tta aaa aag gtg ttc aaa gac agc aaa aaa gac gct tgc   48
Asp Lys Gly Leu Lys Lys Val Phe Lys Asp Ser Lys Lys Asp Ala Cys
 1               5                  10                  15

ggg ttc atc tat gag atc agc gag ttc atg aaa gcc tat acc gca ttg   96
Gly Phe Ile Tyr Glu Ile Ser Glu Phe Met Lys Ala Tyr Thr Ala Leu
            20                  25                  30

cta aaa aaa caa gac cga tac gtc tat tta ttg agg tat ctc ccc tct   144
Leu Lys Lys Gln Asp Arg Tyr Val Tyr Leu Leu Arg Tyr Leu Pro Ser
        35                  40                  45

agg tat tgg gcc agc att tta acg act gcc ctt tat gtc aaa tac cct   192
Arg Tyr Trp Ala Ser Ile Leu Thr Thr Ala Leu Tyr Val Lys Tyr Pro
    50                  55                  60

gat ttt gac gct ttg aaa aag ctt ttg gtg tct tat tat tac caa act   240
Asp Phe Asp Ala Leu Lys Lys Leu Leu Val Ser Tyr Tyr Tyr Gln Thr
65                  70                  75                  80

tgg att gca gga ggc acg atc acg cgc atc aag caa acc agt atc aac   288
Trp Ile Ala Gly Gly Thr Ile Thr Arg Ile Lys Gln Thr Ser Ile Asn
                85                  90                  95

att atc aaa aac gtt aaa agc aat aag agc gtt gaa acc atc aaa gag   336
Ile Ile Lys Asn Val Lys Ser Asn Lys Ser Val Glu Thr Ile Lys Glu
            100                 105                 110

ctt ata ttg aat agc atc gac tct tat aac acc ttt gat caa tac ctc   384
Leu Ile Leu Asn Ser Ile Asp Ser Tyr Asn Thr Phe Asp Gln Tyr Leu
        115                 120                 125

tat aac tta tgg gat agc tct tct gtt tat cat agc aaa tgg gtg cgt   432
Tyr Asn Leu Trp Asp Ser Ser Ser Val Tyr His Ser Lys Trp Val Arg
    130                 135                 140

cct gtc tta gcc cta gct aat tat ttc atg gca gat gaa gag aaa ccc   480
Pro Val Leu Ala Leu Ala Asn Tyr Phe Met Ala Asp Glu Glu Lys Pro
145                 150                 155                 160

cat ttt atc gct atg gat gcc gaa acc caa gtg gag cat att ttg cca   528
His Phe Ile Ala Met Asp Ala Glu Thr Gln Val Glu His Ile Leu Pro
                165                 170                 175

caa acg ccc aaa aga ggc agt caa tgg aac gcg gat ttt gac aaa gaa   576
Gln Thr Pro Lys Arg Gly Ser Gln Trp Asn Ala Asp Phe Asp Lys Glu
            180                 185                 190

aaa aga gaa gaa tgg gta aat aat atc gcg aat tta acc ctt tta aag   624
Lys Arg Glu Glu Trp Val Asn Asn Ile Ala Asn Leu Thr Leu Leu Lys
        195                 200                 205

cgt aaa aag aac gcg cat gct tta aac ggg gat ttt gat gaa aaa aga   672
Arg Lys Lys Asn Ala His Ala Leu Asn Gly Asp Phe Asp Glu Lys Arg
    210                 215                 220

aaa att tat gga ggc aaa gac acg agc aaa gtg att agc tgt tat gac   720
Lys Ile Tyr Gly Gly Lys Asp Thr Ser Lys Val Ile Ser Cys Tyr Asp
225                 230                 235                 240

atc act aaa gaa ttg tat agc aat tat agg aag tgg aat gag aag tcc   768
Ile Thr Lys Glu Leu Tyr Ser Asn Tyr Arg Lys Trp Asn Glu Lys Ser
                245                 250                 255

ctc caa gag cga tac aaa tct ttg tat aac act atc acg cct gtt tta   816
Leu Gln Glu Arg Tyr Lys Ser Leu Tyr Asn Thr Ile Thr Pro Val Leu
            260                 265                 270

cac ata gag ggg caa gaa gat gat ttt gaa gat gat ttt gat cta gaa   864
His Ile Glu Gly Gln Glu Asp Asp Phe Glu Asp Asp Phe Asp Leu Glu
        275                 280                 285
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<210> 192

<211> 288
<212> PRT
<213> Helicobacter pylori
<400> 192

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Asp Lys Gly Leu Lys Lys Val Phe Lys Asp Ser Lys Lys Asp Ala Cys
 1               5                  10                  15
Gly Phe Ile Tyr Glu Ile Ser Glu Phe Met Lys Ala Tyr Thr Ala Leu
            20                  25                  30
Leu Lys Lys Gln Asp Arg Tyr Val Tyr Leu Leu Arg Tyr Leu Pro Ser
        35                  40                  45
Arg Tyr Trp Ala Ser Ile Leu Thr Thr Ala Leu Tyr Val Lys Tyr Pro
    50                  55                  60
Asp Phe Asp Ala Leu Lys Lys Leu Leu Val Ser Tyr Tyr Tyr Gln Thr
65                  70                  75                  80
Trp Ile Ala Gly Gly Thr Ile Thr Arg Ile Lys Gln Thr Ser Ile Asn
                85                  90                  95
Ile Ile Lys Asn Val Lys Ser Asn Lys Ser Val Glu Thr Ile Lys Glu
            100                 105                 110
Leu Ile Leu Asn Ser Ile Asp Ser Tyr Asn Thr Phe Asp Gln Tyr Leu
        115                 120                 125
Tyr Asn Leu Trp Asp Ser Ser Ser Val Tyr His Ser Lys Trp Val Arg
    130                 135                 140
Pro Val Leu Ala Leu Ala Asn Tyr Phe Met Ala Asp Glu Glu Lys Pro
145                 150                 155                 160
His Phe Ile Ala Met Asp Ala Glu Thr Gln Val Glu His Ile Leu Pro
                165                 170                 175
Gln Thr Pro Lys Arg Gly Ser Gln Trp Asn Ala Asp Phe Asp Lys Glu
            180                 185                 190
Lys Arg Glu Glu Trp Val Asn Asn Ile Ala Asn Leu Thr Leu Leu Lys
        195                 200                 205
Arg Lys Lys Asn Ala His Ala Leu Asn Gly Asp Phe Asp Glu Lys Arg
    210                 215                 220
Lys Ile Tyr Gly Gly Lys Asp Thr Ser Lys Val Ile Ser Cys Tyr Asp
225                 230                 235                 240
Ile Thr Lys Glu Leu Tyr Ser Asn Tyr Arg Lys Trp Asn Glu Lys Ser
                245                 250                 255
Leu Gln Glu Arg Tyr Lys Ser Leu Tyr Asn Thr Ile Thr Pro Val Leu
            260                 265                 270
His Ile Glu Gly Gln Glu Asp Asp Phe Glu Asp Asp Phe Asp Leu Glu
        275                 280                 285
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<210> 193
<211> 417
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(417)
<400> 193

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agt gca gaa att ttt gac aag agg gcg ata gac tat gag agc ctc ttt   48
Ser Ala Glu Ile Phe Asp Lys Arg Ala Ile Asp Tyr Glu Ser Leu Phe
 1               5                  10                  15
tca cgc aaa aat agg gcg cga aat ttt atg cca aga atg cca aaa gat   96
Ser Arg Lys Asn Arg Ala Arg Asn Phe Met Pro Arg Met Pro Lys Asp
            20                  25                  30
tcg cac tcg caa ggc ttt gag act tta agc att aat ttt gaa ggc acg  144
Ser His Ser Gln Gly Phe Glu Thr Leu Ser Ile Asn Phe Glu Gly Thr
        35                  40                  45
atg gag tgg agc gcg ttt ggg att tgg ctg agt ttg tta ttg cat caa  192
Met Glu Trp Ser Ala Phe Gly Ile Trp Leu Ser Leu Leu Leu His Gln
    50                  55                  60
tac ggc aca cag att tta cgc atc aag ggg att att gac att gga agc  240
```

```
Tyr Gly Thr Gln Ile Leu Arg Ile Lys Gly Ile Ile Asp Ile Gly Ser
 65                  70                  75                  80
ggc ttt ttg gtg agt att aac ggc gtg atg cat gtc att tac ccg cct   288
Gly Phe Leu Val Ser Ile Asn Gly Val Met His Val Ile Tyr Pro Pro
                 85                  90                  95
aag cat att tta aag gat caa aac ggc tct aac ctc gtt ttt atc atg   336
Lys His Ile Leu Lys Asp Gln Asn Gly Ser Asn Leu Val Phe Ile Met
            100                 105                 110
cgc cat tta gag cgt gaa aaa atc tta aat tcc tta aag ggt ttt aag   384
Arg His Leu Glu Arg Glu Lys Ile Leu Asn Ser Leu Lys Gly Phe Lys
        115                 120                 125
gat ttt ctc ggc atc aag ggt ttt gaa acc caa                      417
Asp Phe Leu Gly Ile Lys Gly Phe Glu Thr Gln
    130                 135
<210> 194
<211> 139
<212> PRT
<213> Helicobacter pylori
<400> 194
Ser Ala Glu Ile Phe Asp Lys Arg Ala Ile Asp Tyr Glu Ser Leu Phe
  1               5                  10                  15
Ser Arg Lys Asn Arg Ala Arg Asn Phe Met Pro Arg Met Pro Lys Asp
             20                  25                  30
Ser His Ser Gln Gly Phe Glu Thr Leu Ser Ile Asn Phe Glu Gly Thr
         35                  40                  45
Met Glu Trp Ser Ala Phe Gly Ile Trp Leu Ser Leu Leu Leu His Gln
     50                  55                  60
Tyr Gly Thr Gln Ile Leu Arg Ile Lys Gly Ile Ile Asp Ile Gly Ser
 65                  70                  75                  80
Gly Phe Leu Val Ser Ile Asn Gly Val Met His Val Ile Tyr Pro Pro
                 85                  90                  95
Lys His Ile Leu Lys Asp Gln Asn Gly Ser Asn Leu Val Phe Ile Met
            100                 105                 110
Arg His Leu Glu Arg Glu Lys Ile Leu Asn Ser Leu Lys Gly Phe Lys
        115                 120                 125
Asp Phe Leu Gly Ile Lys Gly Phe Glu Thr Gln
    130                 135
<210> 195
<211> 615
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(615)
<400> 195
cat tct ttt ggg cta gaa act tac atc cag caa aaa aag gtt acc aat    48
His Ser Phe Gly Leu Glu Thr Tyr Ile Gln Gln Lys Lys Val Thr Asn
  1               5                  10                  15
aaa gaa agc gct tta gaa tat tta aaa gcc aat ctc tct agc cag ttc    96
Lys Glu Ser Ala Leu Glu Tyr Leu Lys Ala Asn Leu Ser Ser Gln Phe
             20                  25                  30
ctt tac acg gaa atg ctg agc ttg aaa tta acc tat gaa agc gcc ctc   144
Leu Tyr Thr Glu Met Leu Ser Leu Lys Leu Thr Tyr Glu Ser Ala Leu
         35                  40                  45
caa caa gat tta aaa aag atc tta ggg gtt gaa gaa gtc att atg cta   192
Gln Gln Asp Leu Lys Lys Ile Leu Gly Val Glu Glu Val Ile Met Leu
     50                  55                  60
tcc aca agc ccc atg gaa tta cga tta gcc aat caa aag ctg ggc aat   240
Ser Thr Ser Pro Met Glu Leu Arg Leu Ala Asn Gln Lys Leu Gly Asn
 65                  70                  75                  80
cgt ttc att aaa acc tta caa gcc atg aac gaa tta gac atg ggc gaa   288
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Arg Phe Ile Lys Thr Leu Gln Ala Met Asn Glu Leu Asp Met Gly Glu
                85                  90                  95
ttt ttt aac gct tac gct caa aaa acc aaa gat ccc acc cat gcc act   336
Phe Phe Asn Ala Tyr Ala Gln Lys Thr Lys Asp Pro Thr His Ala Thr
            100                 105                 110
agc tat ggc gtt ttt gcg gca agt ttg ggg att gaa ttg aaa aag gct   384
Ser Tyr Gly Val Phe Ala Ala Ser Leu Gly Ile Glu Leu Lys Lys Ala
        115                 120                 125
tta agg cat tat ctt tat gcg caa act tct aac atg gtg atc aac tgc   432
Leu Arg His Tyr Leu Tyr Ala Gln Thr Ser Asn Met Val Ile Asn Cys
    130                 135                 140
gtt aaa agc gtc cct tta tct caa aac gac ggg caa aaa atc tta ttg   480
Val Lys Ser Val Pro Leu Ser Gln Asn Asp Gly Gln Lys Ile Leu Leu
145                 150                 155                 160
agc ttg caa agc cct ttt aac cag ctc ata gaa aaa acc cta gaa cta   528
Ser Leu Gln Ser Pro Phe Asn Gln Leu Ile Glu Lys Thr Leu Glu Leu
                165                 170                 175
gac gaa agc cac ctg tgc acg gca agc gtt caa aac gac att aag gcg   576
Asp Glu Ser His Leu Cys Thr Ala Ser Val Gln Asn Asp Ile Lys Ala
            180                 185                 190
atg cag cat gag agt tta tac tcg cgc ctt tat atg tct              615
Met Gln His Glu Ser Leu Tyr Ser Arg Leu Tyr Met Ser
        195                 200                 205
<210> 196
<211> 205
<212> PRT
<213> Helicobacter pylori
<400> 196
His Ser Phe Gly Leu Glu Thr Tyr Ile Gln Gln Lys Lys Val Thr Asn
  1               5                  10                  15
Lys Glu Ser Ala Leu Glu Tyr Leu Lys Ala Asn Leu Ser Ser Gln Phe
            20                  25                  30
Leu Tyr Thr Glu Met Leu Ser Leu Lys Leu Thr Tyr Glu Ser Ala Leu
        35                  40                  45
Gln Gln Asp Leu Lys Lys Ile Leu Gly Val Glu Glu Val Ile Met Leu
    50                  55                  60
Ser Thr Ser Pro Met Glu Leu Arg Leu Ala Asn Gln Lys Leu Gly Asn
65                  70                  75                  80
Arg Phe Ile Lys Thr Leu Gln Ala Met Asn Glu Leu Asp Met Gly Glu
                85                  90                  95
Phe Phe Asn Ala Tyr Ala Gln Lys Thr Lys Asp Pro Thr His Ala Thr
            100                 105                 110
Ser Tyr Gly Val Phe Ala Ala Ser Leu Gly Ile Glu Leu Lys Lys Ala
        115                 120                 125
Leu Arg His Tyr Leu Tyr Ala Gln Thr Ser Asn Met Val Ile Asn Cys
    130                 135                 140
Val Lys Ser Val Pro Leu Ser Gln Asn Asp Gly Gln Lys Ile Leu Leu
145                 150                 155                 160
Ser Leu Gln Ser Pro Phe Asn Gln Leu Ile Glu Lys Thr Leu Glu Leu
                165                 170                 175
Asp Glu Ser His Leu Cys Thr Ala Ser Val Gln Asn Asp Ile Lys Ala
            180                 185                 190
Met Gln His Glu Ser Leu Tyr Ser Arg Leu Tyr Met Ser
        195                 200                 205
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<213> Helicobacter pylori
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<400> 197

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Pro Trp Ala Asn Gly Ser Ile Pro Lys Ser Asn Ser Thr Val Arg Phe
 1               5                  10                  15
ggg ggg tat gag gga gtc aat tgg ggg aaa acg ggc tat att act ggc   96
Gly Gly Tyr Glu Gly Val Asn Trp Gly Lys Thr Gly Tyr Ile Thr Gly
            20                  25                  30
act ttc aca gcc gat agg gtt tat atc acc ggt aac atg atg act ggt   144
Thr Phe Thr Ala Asp Arg Val Tyr Ile Thr Gly Asn Met Met Thr Gly
        35                  40                  45
aac ggc gct caa acc ggt ggg ggg gcg act ttg aat ttt gtg ggc gcg   192
Asn Gly Ala Gln Thr Gly Gly Gly Ala Thr Leu Asn Phe Val Gly Ala
    50                  55                  60
act gaa att aat atc gct gga gcc act ttt aaa aac cta aaa acc act   240
Thr Glu Ile Asn Ile Ala Gly Ala Thr Phe Lys Asn Leu Lys Thr Thr
65                  70                  75                  80
tca caa aac tct tac atg act ttt atg gca tta ggg gat agc tct ggg   288
Ser Gln Asn Ser Tyr Met Thr Phe Met Ala Leu Gly Asp Ser Ser Gly
                85                  90                  95
agc gct aag atc aat gtt tct caa tct gat ttt tac gat tgg acg ggt   336
Ser Ala Lys Ile Asn Val Ser Gln Ser Asp Phe Tyr Asp Trp Thr Gly
            100                 105                 110
ggg ggg tat gat ttt acc ggt aat ggc gtt ttt gat agc gtg aat ttc   384
Gly Gly Tyr Asp Phe Thr Gly Asn Gly Val Phe Asp Ser Val Asn Phe
        115                 120                 125
aac aag gct tat tac aaa ttt caa ggc act gaa aat tct tac aat ttt   432
Asn Lys Ala Tyr Tyr Lys Phe Gln Gly Thr Glu Asn Ser Tyr Asn Phe
    130                 135                 140
aaa aac acg aac ttt tta gca ggg aat ttt aag ttt cag ggc aag acc   480
Lys Asn Thr Asn Phe Leu Ala Gly Asn Phe Lys Phe Gln Gly Lys Thr
145                 150                 155                 160
acc att gaa aaa tcc gtt tta agc gac gct tct tac act ttt gat ggc   528
Thr Ile Glu Lys Ser Val Leu Ser Asp Ala Ser Tyr Thr Phe Asp Gly
                165                 170                 175
acg aat aac acc ttt act gaa gac aag ttt aat aat ggc tcg ttt aat   576
Thr Asn Asn Thr Phe Thr Glu Asp Lys Phe Asn Asn Gly Ser Phe Asn
            180                 185                 190
ttt agt cat gca gag cag aca gac gct ttt aat aac aac tcg ttt aat   624
Phe Ser His Ala Glu Gln Thr Asp Ala Phe Asn Asn Asn Ser Phe Asn
        195                 200                 205
ggc ggt tcg ttt agt ttt aac gcc aag caa gta aat ttt agt ggg aac   672
Gly Gly Ser Phe Ser Phe Asn Ala Lys Gln Val Asn Phe Ser Gly Asn
    210                 215                 220
tcg ttc aat ggg ggc gtg ttt aat ttc aat aat acc cct aaa gtc agt   720
Ser Phe Asn Gly Gly Val Phe Asn Phe Asn Asn Thr Pro Lys Val Ser
225                 230                 235                 240
ttc act gat gac act ttt aat gtg aat aac caa ttc aaa ata aat ggt   768
Phe Thr Asp Asp Thr Phe Asn Val Asn Asn Gln Phe Lys Ile Asn Gly
                245                 250                 255
act caa aca act ttc act ttc aat aag ggc gtt gtt ttc aac atg caa   816
Thr Gln Thr Thr Phe Thr Phe Asn Lys Gly Val Val Phe Asn Met Gln
            260                 265                 270
ggg ctt ttg agc agt tta agc gta ggc acg act tat caa ttg ctt aac   864
Gly Leu Leu Ser Ser Leu Ser Val Gly Thr Thr Tyr Gln Leu Leu Asn
        275                 280                 285
gct aaa agc gtg gat tat aag gat aat aac gct ttg tat caa atg ctg   912
Ala Lys Ser Val Asp Tyr Lys Asp Asn Asn Ala Leu Tyr Gln Met Leu
    290                 295                 300
cgt tgg att agt ggg gaa aac cct agc ggc acg cta gta aat aag gat   960
Arg Trp Ile Ser Gly Glu Asn Pro Ser Gly Thr Leu Val Asn Lys Asp
305                 310                 315                 320
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cag tcc gcg cca aac agc gct aaa att tat aat gtc cat ttc acc gat   1008
Gln Ser Ala Pro Asn Ser Ala Lys Ile Tyr Asn Val His Phe Thr Asp
                325                 330                 335
aac ggc ttg act tac tac atc aaa gaa aat ttt aat aat ggg atc acg   1056
Asn Gly Leu Thr Tyr Tyr Ile Lys Glu Asn Phe Asn Asn Gly Ile Thr
            340                 345                 350
ctc act cgt tta tgc act cta ggc tat acg cat tgc gtg aat att gat   1104
Leu Thr Arg Leu Cys Thr Leu Gly Tyr Thr His Cys Val Asn Ile Asp
        355                 360                 365
aac gat gcg ttt aat ct                                           1121
Asn Asp Ala Phe Asn
    370
<210> 198
<211> 373
<212> PRT
<213> Helicobacter pylori
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Pro Trp Ala Asn Gly Ser Ile Pro Lys Ser Asn Ser Thr Val Arg Phe
  1               5                  10                  15
Gly Gly Tyr Glu Gly Val Asn Trp Gly Lys Thr Gly Tyr Ile Thr Gly
             20                  25                  30
Thr Phe Thr Ala Asp Arg Val Tyr Ile Thr Gly Asn Met Met Thr Gly
         35                  40                  45
Asn Gly Ala Gln Thr Gly Gly Gly Ala Thr Leu Asn Phe Val Gly Ala
     50                  55                  60
Thr Glu Ile Asn Ile Ala Gly Ala Thr Phe Lys Asn Leu Lys Thr Thr
 65                  70                  75                  80
Ser Gln Asn Ser Tyr Met Thr Phe Met Ala Leu Gly Asp Ser Ser Gly
                 85                  90                  95
Ser Ala Lys Ile Asn Val Ser Gln Ser Asp Phe Tyr Asp Trp Thr Gly
            100                 105                 110
Gly Gly Tyr Asp Phe Thr Gly Asn Gly Val Phe Asp Ser Val Asn Phe
        115                 120                 125
Asn Lys Ala Tyr Tyr Lys Phe Gln Gly Thr Glu Asn Ser Tyr Asn Phe
    130                 135                 140
Lys Asn Thr Asn Phe Leu Ala Gly Asn Phe Lys Phe Gln Gly Lys Thr
145                 150                 155                 160
Thr Ile Glu Lys Ser Val Leu Ser Asp Ala Ser Tyr Thr Phe Asp Gly
                165                 170                 175
Thr Asn Asn Thr Phe Thr Glu Asp Lys Phe Asn Asn Gly Ser Phe Asn
            180                 185                 190
Phe Ser His Ala Glu Gln Thr Asp Ala Phe Asn Asn Asn Ser Phe Asn
        195                 200                 205
Gly Gly Ser Phe Ser Phe Asn Ala Lys Gln Val Asn Phe Ser Gly Asn
    210                 215                 220
Ser Phe Asn Gly Gly Val Phe Asn Phe Asn Asn Thr Pro Lys Val Ser
225                 230                 235                 240
Phe Thr Asp Asp Thr Phe Asn Val Asn Asn Gln Phe Lys Ile Asn Gly
                245                 250                 255
Thr Gln Thr Thr Phe Thr Phe Asn Lys Gly Val Val Phe Asn Met Gln
            260                 265                 270
Gly Leu Leu Ser Ser Leu Ser Val Gly Thr Thr Tyr Gln Leu Leu Asn
        275                 280                 285
Ala Lys Ser Val Asp Tyr Lys Asp Asn Asn Ala Leu Tyr Gln Met Leu
    290                 295                 300
Arg Trp Ile Ser Gly Glu Asn Pro Ser Gly Thr Leu Val Asn Lys Asp
305                 310                 315                 320
Gln Ser Ala Pro Asn Ser Ala Lys Ile Tyr Asn Val His Phe Thr Asp
                325                 330                 335
Asn Gly Leu Thr Tyr Tyr Ile Lys Glu Asn Phe Asn Asn Gly Ile Thr
            340                 345                 350
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Leu Thr Arg Leu Cys Thr Leu Gly Tyr Thr His Cys Val Asn Ile Asp
        355                 360                 365
Asn Asp Ala Phe Asn
    370
<210> 199
<211> 679
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(678)
<400> 199
cac gct tac aat aaa gaa gtg gag tta gtt tta agc act aat ggt ttt   48
His Ala Tyr Asn Lys Glu Val Glu Leu Val Leu Ser Thr Asn Gly Phe
  1               5                  10                  15
tta ctc aaa aaa atg gct aag gat tta aaa aat gcc ggg tta gcg caa   96
Leu Leu Lys Lys Met Ala Lys Asp Leu Lys Asn Ala Gly Leu Ala Gln
             20                  25                  30
gtg aat gtt tca ttg gat tct tta aaa agc gat agg gtt tta aaa atc   144
Val Asn Val Ser Leu Asp Ser Leu Lys Ser Asp Arg Val Leu Lys Ile
         35                  40                  45
tct caa aaa gac gct ctt aaa aac acg cta gaa ggg att gaa gag tct   192
Ser Gln Lys Asp Ala Leu Lys Asn Thr Leu Glu Gly Ile Glu Glu Ser
     50                  55                  60
ttg aaa gtg ggt tta aaa ctc aaa tta aac acg gtt gtg ata aaa agc   240
Leu Lys Val Gly Leu Lys Leu Lys Leu Asn Thr Val Val Ile Lys Ser
 65                  70                  75                  80
gtt aat gat gat gaa atc tta gag ctt tta gaa tac gca aaa aat agg   288
Val Asn Asp Asp Glu Ile Leu Glu Leu Leu Glu Tyr Ala Lys Asn Arg
                 85                  90                  95
cat ata caa atc cgc tac att gaa ttt atg gaa aac acg cat gct aaa   336
His Ile Gln Ile Arg Tyr Ile Glu Phe Met Glu Asn Thr His Ala Lys
            100                 105                 110
agt ttg gtt aaa ggc ttg aaa gag cga gaa att tta gat ttg atc gct   384
Ser Leu Val Lys Gly Leu Lys Glu Arg Glu Ile Leu Asp Leu Ile Ala
        115                 120                 125
caa aaa tat caa atc att gag gca gaa aaa ccc aaa caa ggg tct tct   432
Gln Lys Tyr Gln Ile Ile Glu Ala Glu Lys Pro Lys Gln Gly Ser Ser
    130                 135                 140
aaa atc tac acg cta gaa aat ggc tat caa ttt ggc att atc gct ccg   480
Lys Ile Tyr Thr Leu Glu Asn Gly Tyr Gln Phe Gly Ile Ile Ala Pro
145                 150                 155                 160
cat agc gat gat ttt tgc caa tct tgc aat cgt atc cgt ttg gct tct   528
His Ser Asp Asp Phe Cys Gln Ser Cys Asn Arg Ile Arg Leu Ala Ser
                165                 170                 175
gat ggt aag att tgc cca tgt tta tac tat caa gac gcc ata gac gct   576
Asp Gly Lys Ile Cys Pro Cys Leu Tyr Tyr Gln Asp Ala Ile Asp Ala
            180                 185                 190
aaa gag gcg atc atc aat aag gat aca aaa aat ata aaa agg ctt tta   624
Lys Glu Ala Ile Ile Asn Lys Asp Thr Lys Asn Ile Lys Arg Leu Leu
        195                 200                 205
aag caa tct gtc atc aat aaa cca gaa aaa aac atg tgg aat gat aaa   672
Lys Gln Ser Val Ile Asn Lys Pro Glu Lys Asn Met Trp Asn Asp Lys
    210                 215                 220
aac agc g                                                        679
Asn Ser
225
<210> 200
<211> 226
<212> PRT
<213> Helicobacter pylori
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His Ala Tyr Asn Lys Glu Val Glu Leu Val Leu Ser Thr Asn Gly Phe
1 5 10 15
Leu Leu Lys Lys Met Ala Lys Asp Leu Lys Asn Ala Gly Leu Ala Gln
20 25 30
Val Asn Val Ser Leu Asp Ser Leu Lys Ser Asp Arg Val Leu Lys Ile
35 40 45
Ser Gln Lys Asp Ala Leu Lys Asn Thr Leu Glu Gly Ile Glu Glu Ser
50 55 60
Leu Lys Val Gly Leu Lys Leu Lys Leu Asn Thr Val Val Ile Lys Ser
65 70 75 80
Val Asn Asp Asp Glu Ile Leu Glu Leu Leu Glu Tyr Ala Lys Asn Arg
85 90 95
His Ile Gln Ile Arg Tyr Ile Glu Phe Met Glu Asn Thr His Ala Lys
100 105 110
Ser Leu Val Lys Gly Leu Lys Glu Arg Glu Ile Leu Asp Leu Ile Ala
115 120 125
Gln Lys Tyr Gln Ile Ile Glu Ala Glu Lys Pro Lys Gln Gly Ser Ser
130 135 140
Lys Ile Tyr Thr Leu Glu Asn Gly Tyr Gln Phe Gly Ile Ile Ala Pro
145 150 155 160
His Ser Asp Asp Phe Cys Gln Ser Cys Asn Arg Ile Arg Leu Ala Ser
165 170 175
Asp Gly Lys Ile Cys Pro Cys Leu Tyr Tyr Gln Asp Ala Ile Asp Ala
180 185 190
Lys Glu Ala Ile Ile Asn Lys Asp Thr Lys Asn Ile Lys Arg Leu Leu
195 200 205
Lys Gln Ser Val Ile Asn Lys Pro Glu Lys Asn Met Trp Asn Asp Lys
210 215 220
Asn Ser
225

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<211> 486
<212> DNA
<213> Helicobacter pylori
<220>
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<222> (1)..(486)
<400> 201

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ttt ttt gtc ttg gct ttt ata gat tta gcg atc aaa cgc cgc caa tac   48
Phe Phe Val Leu Ala Phe Ile Asp Leu Ala Ile Lys Arg Arg Gln Tyr
 1               5                  10                  15

acc aac tct tta aaa atg act aaa caa gaa gtt aag gac gaa tac aaa   96
Thr Asn Ser Leu Lys Met Thr Lys Gln Glu Val Lys Asp Glu Tyr Lys
            20                  25                  30

cag caa gaa ggg aac cca gaa atc aaa gcc aaa atc cgc caa atg atg  144
Gln Gln Glu Gly Asn Pro Glu Ile Lys Ala Lys Ile Arg Gln Met Met
        35                  40                  45

cta aaa aac gcc acg aat aaa atg atg caa gaa atc cct aaa gcc aat  192
Leu Lys Asn Ala Thr Asn Lys Met Met Gln Glu Ile Pro Lys Ala Asn
    50                  55                  60

gtc gtg gtt act aac ccc acc cat tac gcc gtc gct ctc aaa ttt gat  240
Val Val Val Thr Asn Pro Thr His Tyr Ala Val Ala Leu Lys Phe Asp
65                  70                  75                  80

gaa gaa cac cct gtg cct gtg gta gtg gct aaa ggc acg gat tat tta  288
Glu Glu His Pro Val Pro Val Val Val Ala Lys Gly Thr Asp Tyr Leu
                85                  90                  95

gcc att agg att aag ggc atc gct aga gag cat gac ata gaa att ata  336
Ala Ile Arg Ile Lys Gly Ile Ala Arg Glu His Asp Ile Glu Ile Ile
            100                 105                 110

gaa aat aaa acg ctc gcc aga gag ctt tat aga gat gtg aaa tta aac  384
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Glu Asn Lys Thr Leu Ala Arg Glu Leu Tyr Arg Asp Val Lys Leu Asn
        115                 120                 125
gct gcc ata cca gaa gaa ttg ttt gaa gcc gtg gcg ata gtc ttc gct   432
Ala Ala Ile Pro Glu Glu Leu Phe Glu Ala Val Ala Ile Val Phe Ala
    130                 135                 140
caa gtg gct aaa tta gag caa gaa cgc caa aaa caa aag atc att aaa   480
Gln Val Ala Lys Leu Glu Gln Glu Arg Gln Lys Gln Lys Ile Ile Lys
145                 150                 155                 160
cct ctt                                                          486
Pro Leu
<210> 202
<211> 162
<212> PRT
<213> Helicobacter pylori
<400> 202
Phe Phe Val Leu Ala Phe Ile Asp Leu Ala Ile Lys Arg Arg Gln Tyr
  1               5                  10                  15
Thr Asn Ser Leu Lys Met Thr Lys Gln Glu Val Lys Asp Glu Tyr Lys
             20                  25                  30
Gln Gln Glu Gly Asn Pro Glu Ile Lys Ala Lys Ile Arg Gln Met Met
         35                  40                  45
Leu Lys Asn Ala Thr Asn Lys Met Met Gln Glu Ile Pro Lys Ala Asn
     50                  55                  60
Val Val Val Thr Asn Pro Thr His Tyr Ala Val Ala Leu Lys Phe Asp
 65                  70                  75                  80
Glu Glu His Pro Val Pro Val Val Val Ala Lys Gly Thr Asp Tyr Leu
                 85                  90                  95
Ala Ile Arg Ile Lys Gly Ile Ala Arg Glu His Asp Ile Glu Ile Ile
            100                 105                 110
Glu Asn Lys Thr Leu Ala Arg Glu Leu Tyr Arg Asp Val Lys Leu Asn
        115                 120                 125
Ala Ala Ile Pro Glu Glu Leu Phe Glu Ala Val Ala Ile Val Phe Ala
    130                 135                 140
Gln Val Ala Lys Leu Glu Gln Glu Arg Gln Lys Gln Lys Ile Ile Lys
145                 150                 155                 160
Pro Leu

<210> 203
<211> 174
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(174)
<400> 203
acc gga aga acc cat caa atc aga gtc cat tta aag cat atc aac cac   48
Thr Gly Arg Thr His Gln Ile Arg Val His Leu Lys His Ile Asn His
  1               5                  10                  15
ccc att ata ggc gat acg ctt tat aat aac gag cca agt tta gcc aaa   96
Pro Ile Ile Gly Asp Thr Leu Tyr Asn Asn Glu Pro Ser Leu Ala Lys
             20                  25                  30
cgc ttg atg ctc cat gca cat aaa atc gcg cta cta ggg tat gaa ttt   144
Arg Leu Met Leu His Ala His Lys Ile Ala Leu Leu Gly Tyr Glu Phe
         35                  40                  45
gaa gcg atc gct cct aaa gaa ttt gaa att                          174
Glu Ala Ile Ala Pro Lys Glu Phe Glu Ile
     50                  55
<210> 204
<211> 58
<212> PRT
<213> Helicobacter pylori
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<400> 204
Thr Gly Arg Thr His Gln Ile Arg Val His Leu Lys His Ile Asn His
1 5 10 15
Pro Ile Ile Gly Asp Thr Leu Tyr Asn Asn Glu Pro Ser Leu Ala Lys
20 25 30
Arg Leu Met Leu His Ala His Lys Ile Ala Leu Leu Gly Tyr Glu Phe
35 40 45
Glu Ala Ile Ala Pro Lys Glu Phe Glu Ile
50 55
<210> 205
<211> 69
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(69)
<400> 205
caa gaa atg cac att ctt atg atc cac atc tta tgc gat tgc att gaa 48
Gln Glu Met His Ile Leu Met Ile His Ile Leu Cys Asp Cys Ile Glu
1 5 10 15
agg cat ttc gct cat aaa aat 69
Arg His Phe Ala His Lys Asn
20

<210> 206
<211> 23
<212> PRT
<213> Helicobacter pylori
<400> 206
Gln Glu Met His Ile Leu Met Ile His Ile Leu Cys Asp Cys Ile Glu
1 5 10 15
Arg His Phe Ala His Lys Asn
20

<210> 207
<211> 423
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(423)
<400> 207
agg cat tat gaa acg atg ttt att ctc aaa cct act tta gta gaa gaa 48
Arg His Tyr Glu Thr Met Phe Ile Leu Lys Pro Thr Leu Val Glu Glu
1 5 10 15
gag att aaa tcc aag att gag ttt tat aaa gaa gtg atc act aag cat 96
Glu Ile Lys Ser Lys Ile Glu Phe Tyr Lys Glu Val Ile Thr Lys His
20 25 30
cac ggc gtg att gaa acg agc ctg gat atg ggc atg cgt aat tta gct 144
His Gly Val Ile Glu Thr Ser Leu Asp Met Gly Met Arg Asn Leu Ala
35 40 45
tat gaa atc aaa aag cac aaa aga ggc tat tat tat gtg gcg tat ttc 192
Tyr Glu Ile Lys Lys His Lys Arg Gly Tyr Tyr Tyr Val Ala Tyr Phe
50 55 60
aaa gcg gag ccg tca atg att gta gag ctt gaa cga ttg tat cgc atc 240
Lys Ala Glu Pro Ser Met Ile Val Glu Leu Glu Arg Leu Tyr Arg Ile
65 70 75 80
aat gaa gac gtg ttg cgt ttc att gtg atc aaa tac gaa agc aag aaa 288
Asn Glu Asp Val Leu Arg Phe Ile Val Ile Lys Tyr Glu Ser Lys Lys
85 90 95
gaa gtg gaa gcg tgg cat gcg ttg gtg gat agg gct aat aaa aag cca 336
Glu Val Glu Ala Trp His Ala Leu Val Asp Arg Ala Asn Lys Lys Pro
100 105 110

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tcg cac gcc aaa gaa aaa cac gaa aaa acc gaa cac acg cat tct cac   384
Ser His Ala Lys Glu Lys His Glu Lys Thr Glu His Thr His Ser His
        115                 120                 125
cac aca gag gaa gca gaa agc gta gga tct cat agc gaa               423
His Thr Glu Glu Ala Glu Ser Val Gly Ser His Ser Glu
    130                 135                 140
<210> 208
<211> 141
<212> PRT
<213> Helicobacter pylori
<400> 208
Arg His Tyr Glu Thr Met Phe Ile Leu Lys Pro Thr Leu Val Glu Glu
  1               5                  10                  15
Glu Ile Lys Ser Lys Ile Glu Phe Tyr Lys Glu Val Ile Thr Lys His
            20                  25                  30
His Gly Val Ile Glu Thr Ser Leu Asp Met Gly Met Arg Asn Leu Ala
        35                  40                  45
Tyr Glu Ile Lys Lys His Lys Arg Gly Tyr Tyr Tyr Val Ala Tyr Phe
    50                  55                  60
Lys Ala Glu Pro Ser Met Ile Val Glu Leu Glu Arg Leu Tyr Arg Ile
65                  70                  75                  80
Asn Glu Asp Val Leu Arg Phe Ile Val Ile Lys Tyr Glu Ser Lys Lys
                85                  90                  95
Glu Val Glu Ala Trp His Ala Leu Val Asp Arg Ala Asn Lys Lys Pro
            100                 105                 110
Ser His Ala Lys Glu Lys His Glu Lys Thr Glu His Thr His Ser His
        115                 120                 125
His Thr Glu Glu Ala Glu Ser Val Gly Ser His Ser Glu
    130                 135                 140
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<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)...(210)
<400> 209
tca agc gat aac ccg cta gcc gat gag ccg gat ttg gat tac gct aac   48
Ser Ser Asp Asn Pro Leu Ala Asp Glu Pro Asp Leu Asp Tyr Ala Asn
  1               5                  10                  15
atg agc gct gaa gaa gtg gaa gca gag att gaa cgg ctg ctg aac aaa   96
Met Ser Ala Glu Glu Val Glu Ala Glu Ile Glu Arg Leu Leu Asn Lys
            20                  25                  30
cgc caa gaa gcc gat aaa gaa cga aga gct caa aaa aaa caa gaa gcc   144
Arg Gln Glu Ala Asp Lys Glu Arg Arg Ala Gln Lys Lys Gln Glu Ala
        35                  40                  45
aaa ccc aaa caa gaa gtt acc cca aca aaa gaa acc ccc aaa gcc cct   192
Lys Pro Lys Gln Glu Val Thr Pro Thr Lys Glu Thr Pro Lys Ala Pro
    50                  55                  60
aaa acc gaa act aaa gct aa                                      212
Lys Thr Glu Thr Lys Ala
65                  70
<210> 210
<211> 70
<212> PRT
<213> Helicobacter pylori
<400> 210
Ser Ser Asp Asn Pro Leu Ala Asp Glu Pro Asp Leu Asp Tyr Ala Asn
  1               5                  10                  15
Met Ser Ala Glu Glu Val Glu Ala Glu Ile Glu Arg Leu Leu Asn Lys
            20                  25                  30
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Arg Gln Glu Ala Asp Lys Glu Arg Arg Ala Gln Lys Lys Gln Glu Ala
         35                  40                  45
Lys Pro Lys Gln Glu Val Thr Pro Thr Lys Glu Thr Pro Lys Ala Pro
     50                  55                  60
Lys Thr Glu Thr Lys Ala
 65                  70
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<211> 798
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(798)
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gca gaa gaa agt aaa ggg agt gtt gca aaa tat aaa ata gaa gct caa   48
Ala Glu Glu Ser Lys Gly Ser Val Ala Lys Tyr Lys Ile Glu Ala Gln
  1               5                  10                  15
tac agc att gat ttt gat tct gca gaa cac act tca ctt ttc att ccc   96
Tyr Ser Ile Asp Phe Asp Ser Ala Glu His Thr Ser Leu Phe Ile Pro
             20                  25                  30
atg ccg agt gtt gta gcg agc aat gtg cat tta caa ggc aat cat gct   144
Met Pro Ser Val Val Ala Ser Asn Val His Leu Gln Gly Asn His Ala
         35                  40                  45
agc tat aaa agc atg ctc aat ttt gga gtg cct tat ttg caa gtg gat   192
Ser Tyr Lys Ser Met Leu Asn Phe Gly Val Pro Tyr Leu Gln Val Asp
     50                  55                  60
ttt tta aaa agc act caa aaa aag caa gtc cat ttg tct tat gag atc   240
Phe Leu Lys Ser Thr Gln Lys Lys Gln Val His Leu Ser Tyr Glu Ile
 65                  70                  75                  80
gct agc tat caa ttg aat gag cgt ttg ttt gaa acg agc gat ttt gta   288
Ala Ser Tyr Gln Leu Asn Glu Arg Leu Phe Glu Thr Ser Asp Phe Val
                 85                  90                  95
gca atg ggg cgt tat gaa aga gac gat gcg agc gtg gct aac att gcc   336
Ala Met Gly Arg Tyr Glu Arg Asp Asp Ala Ser Val Ala Asn Ile Ala
            100                 105                 110
aac cag ctt aag gga aca acc cct aaa gaa agc gtt cgc aat ttt tat   384
Asn Gln Leu Lys Gly Thr Thr Pro Lys Glu Ser Val Arg Asn Phe Tyr
        115                 120                 125
gcg ttc atc aag cat gag atg cct aag aga cag aag gct tta gag ggt   432
Ala Phe Ile Lys His Glu Met Pro Lys Arg Gln Lys Ala Leu Glu Gly
    130                 135                 140
aaa gaa aat tta cct aag cgt gag agt ttg ccc tgg ttt gca acc att   480
Lys Glu Asn Leu Pro Lys Arg Glu Ser Leu Pro Trp Phe Ala Thr Ile
145                 150                 155                 160
tca aaa gag agc atg ttt gtg tcc tta tgc cat gcg tgc ggg att aaa   528
Ser Lys Glu Ser Met Phe Val Ser Leu Cys His Ala Cys Gly Ile Lys
                165                 170                 175
agc gct gaa gtg caa ggc ttg aaa ctg ggt caa aac agc gtg gtg aaa   576
Ser Ala Glu Val Gln Gly Leu Lys Leu Gly Gln Asn Ser Val Val Lys
            180                 185                 190
aac gct cct aga gtg gaa gtg tat ttg aaa gat tca ttt cta gcg ttt   624
Asn Ala Pro Arg Val Glu Val Tyr Leu Lys Asp Ser Phe Leu Ala Phe
        195                 200                 205
gat ttt caa aat aat cac aag gaa gtt ttt atc ccg ttg aat cgt cat   672
Asp Phe Gln Asn Asn His Lys Glu Val Phe Ile Pro Leu Asn Arg His
    210                 215                 220
aaa gac atg cag tta gat tct gcc tta ttg gcg act ttt ggc gat gct   720
Lys Asp Met Gln Leu Asp Ser Ala Leu Leu Ala Thr Phe Gly Asp Ala
225                 230                 235                 240
ttt gcc ctt gtg gat ggt agg gat tta ggc aat tac gag agc aaa ctt   768
Phe Ala Leu Val Asp Gly Arg Asp Leu Gly Asn Tyr Glu Ser Lys Leu
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245 250 255

ttt gaa aaa aga gtg tcc tat acg att gtc 798
Phe Glu Lys Arg Val Ser Tyr Thr Ile Val
260 265

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<211> 266
<212> PRT
<213> Helicobacter pylori
<400> 212
Ala Glu Glu Ser Lys Gly Ser Val Ala Lys Tyr Lys Ile Glu Ala Gln
1 5 10 15
Tyr Ser Ile Asp Phe Asp Ser Ala Glu His Thr Ser Leu Phe Ile Pro
20 25 30
Met Pro Ser Val Val Ala Ser Asn Val His Leu Gln Gly Asn His Ala
35 40 45
Ser Tyr Lys Ser Met Leu Asn Phe Gly Val Pro Tyr Leu Gln Val Asp
50 55 60
Phe Leu Lys Ser Thr Gln Lys Lys Gln Val His Leu Ser Tyr Glu Ile
65 70 75 80
Ala Ser Tyr Gln Leu Asn Glu Arg Leu Phe Glu Thr Ser Asp Phe Val
85 90 95
Ala Met Gly Arg Tyr Glu Arg Asp Asp Ala Ser Val Ala Asn Ile Ala
100 105 110
Asn Gln Leu Lys Gly Thr Thr Pro Lys Glu Ser Val Arg Asn Phe Tyr
115 120 125
Ala Phe Ile Lys His Glu Met Pro Lys Arg Gln Lys Ala Leu Glu Gly
130 135 140
Lys Glu Asn Leu Pro Lys Arg Glu Ser Leu Pro Trp Phe Ala Thr Ile
145 150 155 160
Ser Lys Glu Ser Met Phe Val Ser Leu Cys His Ala Cys Gly Ile Lys
165 170 175
Ser Ala Glu Val Gln Gly Leu Lys Leu Gly Gln Asn Ser Val Val Lys
180 185 190
Asn Ala Pro Arg Val Glu Val Tyr Leu Lys Asp Ser Phe Leu Ala Phe
195 200 205
Asp Phe Gln Asn Asn His Lys Glu Val Phe Ile Pro Leu Asn Arg His
210 215 220
Lys Asp Met Gln Leu Asp Ser Ala Leu Leu Ala Thr Phe Gly Asp Ala
225 230 235 240
Phe Ala Leu Val Asp Gly Arg Asp Leu Gly Asn Tyr Glu Ser Lys Leu
245 250 255
Phe Glu Lys Arg Val Ser Tyr Thr Ile Val
260 265

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<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(168)
<400> 213
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Cys Met Phe Asp Gly Tyr Thr His Tyr Leu Asn Leu Val Leu Val Asn
1 5 10 15
tgc ccc ata gag ctc tct ggt gtg cga gaa tgc att gaa gaa agc gaa 96
Cys Pro Ile Glu Leu Ser Gly Val Arg Glu Cys Ile Glu Glu Ser Glu
20 25 30
ggg gtg gat ggg gca gtg agt gaa acc gct agt tct cat tta tgc gtg 144
Gly Val Asp Gly Ala Val Ser Glu Thr Ala Ser Ser His Leu Cys Val
35 40 45
aaa gct tta gcg aaa ggc tca gaa cc 170

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Lys Ala Leu Ala Lys Gly Ser Glu
     50                  55
<210> 214
<211> 56
<212> PRT
<213> Helicobacter pylori
<400> 214
Cys Met Phe Asp Gly Tyr Thr His Tyr Leu Asn Leu Val Leu Val Asn
  1               5                  10                  15
Cys Pro Ile Glu Leu Ser Gly Val Arg Glu Cys Ile Glu Glu Ser Glu
             20                  25                  30
Gly Val Asp Gly Ala Val Ser Glu Thr Ala Ser Ser His Leu Cys Val
         35                  40                  45
Lys Ala Leu Ala Lys Gly Ser Glu
     50                  55
<210> 215
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<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(717)
<400> 215
ggc ggg att gcg tgc gcg aat ttg ttg cat aaa aat tca ggg atc acg   48
Gly Gly Ile Ala Cys Ala Asn Leu Leu His Lys Asn Ser Gly Ile Thr
  1               5                  10                  15
ata gat att gga ggg ggt agc acc gag tgc gcg ttg att gaa aaa ggc   96
Ile Asp Ile Gly Gly Gly Ser Thr Glu Cys Ala Leu Ile Glu Lys Gly
             20                  25                  30
aag att aag gac tta atc tcg ctt gat gtt ggg acg att cgc att aaa   144
Lys Ile Lys Asp Leu Ile Ser Leu Asp Val Gly Thr Ile Arg Ile Lys
         35                  40                  45
gaa atg ttt tta gac aaa gac tta gag gtc aaa ttg gct aaa gcc ttt   192
Glu Met Phe Leu Asp Lys Asp Leu Glu Val Lys Leu Ala Lys Ala Phe
     50                  55                  60
atc caa aaa gaa gtc tct aaa ctg ccc ttt aaa cac aaa aac gcc ttt   240
Ile Gln Lys Glu Val Ser Lys Leu Pro Phe Lys His Lys Asn Ala Phe
 65                  70                  75                  80
ggg gtg ggg ggg acg atc aga gcg ttg agt aag gta ttg atg aaa cgc   288
Gly Val Gly Gly Thr Ile Arg Ala Leu Ser Lys Val Leu Met Lys Arg
                 85                  90                  95
ttt tgt tac cct att gat tct ttg cat ggc tat gaa ata gat gca cat   336
Phe Cys Tyr Pro Ile Asp Ser Leu His Gly Tyr Glu Ile Asp Ala His
            100                 105                 110
aaa aat tta gcg ttc att gaa aaa atc gtc atg ctc aaa gaa gat caa   384
Lys Asn Leu Ala Phe Ile Glu Lys Ile Val Met Leu Lys Glu Asp Gln
        115                 120                 125
tta cgg ctt tta ggg gtg aat gaa gag cgt ttg gat agc atc agg agc   432
Leu Arg Leu Leu Gly Val Asn Glu Glu Arg Leu Asp Ser Ile Arg Ser
    130                 135                 140
ggg gcg ttg att tta tca gtc gtt ttg gag cat tta aaa act tct tta   480
Gly Ala Leu Ile Leu Ser Val Val Leu Glu His Leu Lys Thr Ser Leu
145                 150                 155                 160
atg atc act agt ggg gtg ggg gtg aga gaa ggc gtg ttt ttg agc gat   528
Met Ile Thr Ser Gly Val Gly Val Arg Glu Gly Val Phe Leu Ser Asp
                165                 170                 175
tta ttg cgc cat cat tac cat aaa ttc ccc ccc aat atc aac ccc tct   576
Leu Leu Arg His His Tyr His Lys Phe Pro Pro Asn Ile Asn Pro Ser
            180                 185                 190
ctc atc tct tta aaa gat cgc ttt ttg ccc cat gaa aag cac agc caa   624
Leu Ile Ser Leu Lys Asp Arg Phe Leu Pro His Glu Lys His Ser Gln
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       195                 200                 205
aag gtc aaa aaa gaa tgc gtg aaa ttg ttt gaa gcc tta tcg cct ttg   672
Lys Val Lys Lys Glu Cys Val Lys Leu Phe Glu Ala Leu Ser Pro Leu
    210                 215                 220
cat aaa ata gat gaa aaa tac ctt ttc cat tta aag att gcg ggg       717
His Lys Ile Asp Glu Lys Tyr Leu Phe His Leu Lys Ile Ala Gly
225                 230                 235
<210> 216
<211> 239
<212> PRT
<213> Helicobacter pylori
<400> 216
Gly Gly Ile Ala Cys Ala Asn Leu Leu His Lys Asn Ser Gly Ile Thr
  1               5                  10                  15
Ile Asp Ile Gly Gly Gly Ser Thr Glu Cys Ala Leu Ile Glu Lys Gly
            20                  25                  30
Lys Ile Lys Asp Leu Ile Ser Leu Asp Val Gly Thr Ile Arg Ile Lys
        35                  40                  45
Glu Met Phe Leu Asp Lys Asp Leu Glu Val Lys Leu Ala Lys Ala Phe
    50                  55                  60
Ile Gln Lys Glu Val Ser Lys Leu Pro Phe Lys His Lys Asn Ala Phe
65                  70                  75                  80
Gly Val Gly Gly Thr Ile Arg Ala Leu Ser Lys Val Leu Met Lys Arg
                85                  90                  95
Phe Cys Tyr Pro Ile Asp Ser Leu His Gly Tyr Glu Ile Asp Ala His
            100                 105                 110
Lys Asn Leu Ala Phe Ile Glu Lys Ile Val Met Leu Lys Glu Asp Gln
        115                 120                 125
Leu Arg Leu Leu Gly Val Asn Glu Glu Arg Leu Asp Ser Ile Arg Ser
    130                 135                 140
Gly Ala Leu Ile Leu Ser Val Val Leu Glu His Leu Lys Thr Ser Leu
145                 150                 155                 160
Met Ile Thr Ser Gly Val Gly Val Arg Glu Gly Val Phe Leu Ser Asp
                165                 170                 175
Leu Leu Arg His His Tyr His Lys Phe Pro Pro Asn Ile Asn Pro Ser
            180                 185                 190
Leu Ile Ser Leu Lys Asp Arg Phe Leu Pro His Glu Lys His Ser Gln
        195                 200                 205
Lys Val Lys Lys Glu Cys Val Lys Leu Phe Glu Ala Leu Ser Pro Leu
    210                 215                 220
His Lys Ile Asp Glu Lys Tyr Leu Phe His Leu Lys Ile Ala Gly
225                 230                 235
<210> 217
<211> 480
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(480)
<400> 217
tct tct tta caa agc gaa cac atc aat tcc ccc ctt gtc cca gaa gcg   48
Ser Ser Leu Gln Ser Glu His Ile Asn Ser Pro Leu Val Pro Glu Ala
  1               5                  10                  15
atg cta gct tta ggg caa gcg cac atg aaa aag aaa gag tat gtt tta   96
Met Leu Ala Leu Gly Gln Ala His Met Lys Lys Lys Glu Tyr Val Leu
            20                  25                  30
gcg tct ttt tac ttt gat gaa tac atc aag cgc ttt ggg act aag gac   144
Ala Ser Phe Tyr Phe Asp Glu Tyr Ile Lys Arg Phe Gly Thr Lys Asp
        35                  40                  45
aat gtg gat tat ttg act ttt tta aaa ttg caa tcg cat tat tac gct   192
Asn Val Asp Tyr Leu Thr Phe Leu Lys Leu Gln Ser His Tyr Tyr Ala
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    50                  55                  60
ttc aaa aac cat tct aaa gac cag gaa ttt atc tct aat tct att gtg   240
Phe Lys Asn His Ser Lys Asp Gln Glu Phe Ile Ser Asn Ser Ile Val
 65                  70                  75                  80
agt tta ggc gaa ttt ata gaa aaa tac cct aac agc cgt tac cgc ccc   288
Ser Leu Gly Glu Phe Ile Glu Lys Tyr Pro Asn Ser Arg Tyr Arg Pro
                85                  90                  95
tat gta gaa tac atg caa atc aaa ttc att tta ggg caa aat gag ctc   336
Tyr Val Glu Tyr Met Gln Ile Lys Phe Ile Leu Gly Gln Asn Glu Leu
            100                 105                 110
aat cgc gcg atc gcg aat gtc tat aaa aaa cgc cac aag cct gag ggc   384
Asn Arg Ala Ile Ala Asn Val Tyr Lys Lys Arg His Lys Pro Glu Gly
        115                 120                 125
gtg aaa cgc tat tta gaa agg ata gat gag act tta gaa aaa gag act   432
Val Lys Arg Tyr Leu Glu Arg Ile Asp Glu Thr Leu Glu Lys Glu Thr
    130                 135                 140
aaa ccc aaa cca tcg cac atg cct tgg tat gtg tta att ttt gat tgg   480
Lys Pro Lys Pro Ser His Met Pro Trp Tyr Val Leu Ile Phe Asp Trp
145                 150                 155                 160
<210> 218
<211> 160
<212> PRT
<213> Helicobacter pylori
<400> 218
Ser Ser Leu Gln Ser Glu His Ile Asn Ser Pro Leu Val Pro Glu Ala
  1               5                  10                  15
Met Leu Ala Leu Gly Gln Ala His Met Lys Lys Lys Glu Tyr Val Leu
            20                  25                  30
Ala Ser Phe Tyr Phe Asp Glu Tyr Ile Lys Arg Phe Gly Thr Lys Asp
        35                  40                  45
Asn Val Asp Tyr Leu Thr Phe Leu Lys Leu Gln Ser His Tyr Tyr Ala
    50                  55                  60
Phe Lys Asn His Ser Lys Asp Gln Glu Phe Ile Ser Asn Ser Ile Val
65                  70                  75                  80
Ser Leu Gly Glu Phe Ile Glu Lys Tyr Pro Asn Ser Arg Tyr Arg Pro
                85                  90                  95
Tyr Val Glu Tyr Met Gln Ile Lys Phe Ile Leu Gly Gln Asn Glu Leu
            100                 105                 110
Asn Arg Ala Ile Ala Asn Val Tyr Lys Lys Arg His Lys Pro Glu Gly
        115                 120                 125
Val Lys Arg Tyr Leu Glu Arg Ile Asp Glu Thr Leu Glu Lys Glu Thr
    130                 135                 140
Lys Pro Lys Pro Ser His Met Pro Trp Tyr Val Leu Ile Phe Asp Trp
145                 150                 155                 160
<210> 219
<211> 814
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(813)
<400> 219
gac agc aaa aaa gac gct tgc ggg ttc atc tat gag atc agc gag ttc    48
Asp Ser Lys Lys Asp Ala Cys Gly Phe Ile Tyr Glu Ile Ser Glu Phe
  1               5                  10                  15
atg aaa gcc tat acc gca ttg cta aaa aaa caa gac cga tac gtc tat    96
Met Lys Ala Tyr Thr Ala Leu Leu Lys Lys Gln Asp Arg Tyr Val Tyr
            20                  25                  30
tta ttg agg tat ctc ccc tct agg tat tgg gcc agc att tta acg act   144
Leu Leu Arg Tyr Leu Pro Ser Arg Tyr Trp Ala Ser Ile Leu Thr Thr
        35                  40                  45
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gcc ctt tat gtc aaa tac cct gat ttt gac gct ttg aaa aag ctt ttg   192
Ala Leu Tyr Val Lys Tyr Pro Asp Phe Asp Ala Leu Lys Lys Leu Leu
     50                  55                  60
gtg tct tat tat tac caa act tgg att gca gga ggc acg atc acg cgc   240
Val Ser Tyr Tyr Tyr Gln Thr Trp Ile Ala Gly Gly Thr Ile Thr Arg
 65                  70                  75                  80
atc aag caa acc agt atc aac att atc aaa aac gtt aaa agc aat aag   288
Ile Lys Gln Thr Ser Ile Asn Ile Ile Lys Asn Val Lys Ser Asn Lys
                 85                  90                  95
agc gtt gaa acc atc aaa gag ctt ata ttg aat agc atc gac tct tat   336
Ser Val Glu Thr Ile Lys Glu Leu Ile Leu Asn Ser Ile Asp Ser Tyr
            100                 105                 110
aac acc ttt gat caa tac ctc tat aac tta tgg gat agc tct tct gtt   384
Asn Thr Phe Asp Gln Tyr Leu Tyr Asn Leu Trp Asp Ser Ser Ser Val
        115                 120                 125
tat cat agc aaa tgg gtg cgt cct gtc tta gcc cta gct aat tat ttc   432
Tyr His Ser Lys Trp Val Arg Pro Val Leu Ala Leu Ala Asn Tyr Phe
    130                 135                 140
atg gca gat gaa gag aaa ccc cat ttt atc gct atg gat gcc gaa acc   480
Met Ala Asp Glu Glu Lys Pro His Phe Ile Ala Met Asp Ala Glu Thr
145                 150                 155                 160
caa gtg gag cat att ttg cca caa acg ccc aaa aga ggc agt caa tgg   528
Gln Val Glu His Ile Leu Pro Gln Thr Pro Lys Arg Gly Ser Gln Trp
                165                 170                 175
aac gcg gat ttt gac aaa gaa aaa aga gaa gaa tgg gta aat aat atc   576
Asn Ala Asp Phe Asp Lys Glu Lys Arg Glu Glu Trp Val Asn Asn Ile
            180                 185                 190
gcg aat tta acc ctt tta aag cgt aaa aag aac gcg cat gct tta aac   624
Ala Asn Leu Thr Leu Leu Lys Arg Lys Lys Asn Ala His Ala Leu Asn
        195                 200                 205
ggg gat ttt gat gaa aaa aga aaa att tat gga ggc aaa gac acg agc   672
Gly Asp Phe Asp Glu Lys Arg Lys Ile Tyr Gly Gly Lys Asp Thr Ser
    210                 215                 220
aaa gtg att agc tgt tat gac atc act aaa gaa ttg tat agc aat tat   720
Lys Val Ile Ser Cys Tyr Asp Ile Thr Lys Glu Leu Tyr Ser Asn Tyr
225                 230                 235                 240
agg aag tgg aat gag aag tcc ctc caa gag cga tac aaa tct ttg tat   768
Arg Lys Trp Asn Glu Lys Ser Leu Gln Glu Arg Tyr Lys Ser Leu Tyr
                245                 250                 255
aac act atc acg cct gtt tta cac ata gag ggg caa gaa gat gat t     814
Asn Thr Ile Thr Pro Val Leu His Ile Glu Gly Gln Glu Asp Asp
            260                 265                 270
<210> 220
<211> 271
<212> PRT
<213> Helicobacter pylori
<400> 220
Asp Ser Lys Lys Asp Ala Cys Gly Phe Ile Tyr Glu Ile Ser Glu Phe
  1               5                  10                  15
Met Lys Ala Tyr Thr Ala Leu Leu Lys Lys Gln Asp Arg Tyr Val Tyr
            20                  25                  30
Leu Leu Arg Tyr Leu Pro Ser Arg Tyr Trp Ala Ser Ile Leu Thr Thr
        35                  40                  45
Ala Leu Tyr Val Lys Tyr Pro Asp Phe Asp Ala Leu Lys Lys Leu Leu
    50                  55                  60
Val Ser Tyr Tyr Tyr Gln Thr Trp Ile Ala Gly Gly Thr Ile Thr Arg
 65                  70                  75                  80
Ile Lys Gln Thr Ser Ile Asn Ile Ile Lys Asn Val Lys Ser Asn Lys
                85                  90                  95
Ser Val Glu Thr Ile Lys Glu Leu Ile Leu Asn Ser Ile Asp Ser Tyr
            100                 105                 110
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Asn Thr Phe Asp Gln Tyr Leu Tyr Asn Leu Trp Asp Ser Ser Ser Val
        115                 120                 125
Tyr His Ser Lys Trp Val Arg Pro Val Leu Ala Leu Ala Asn Tyr Phe
    130                 135                 140
Met Ala Asp Glu Glu Lys Pro His Phe Ile Ala Met Asp Ala Glu Thr
145                 150                 155                 160
Gln Val Glu His Ile Leu Pro Gln Thr Pro Lys Arg Gly Ser Gln Trp
                165                 170                 175
Asn Ala Asp Phe Asp Lys Glu Lys Arg Glu Glu Trp Val Asn Asn Ile
            180                 185                 190
Ala Asn Leu Thr Leu Leu Lys Arg Lys Lys Asn Ala His Ala Leu Asn
        195                 200                 205
Gly Asp Phe Asp Glu Lys Arg Lys Ile Tyr Gly Gly Lys Asp Thr Ser
    210                 215                 220
Lys Val Ile Ser Cys Tyr Asp Ile Thr Lys Glu Leu Tyr Ser Asn Tyr
225                 230                 235                 240
Arg Lys Trp Asn Glu Lys Ser Leu Gln Glu Arg Tyr Lys Ser Leu Tyr
                245                 250                 255
Asn Thr Ile Thr Pro Val Leu His Ile Glu Gly Gln Glu Asp Asp
            260                 265                 270
<210> 221
<211> 648
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(648)
<400> 221
aag tat atc aat tcg ccc caa agt aag ctt ttt gat aaa tcc agt ttg   48
Lys Tyr Ile Asn Ser Pro Gln Ser Lys Leu Phe Asp Lys Ser Ser Leu
  1               5                  10                  15
ctc tat ggc tat cat ttg gct aaa gaa cac atc tat aaa caa aag caa   96
Leu Tyr Gly Tyr His Leu Ala Lys Glu His Ile Tyr Lys Gln Lys Gln
             20                  25                  30
gtc att gta aca gag ggg tat ttg gat gtg att tta ttg cac cag gcg   144
Val Ile Val Thr Glu Gly Tyr Leu Asp Val Ile Leu Leu His Gln Ala
         35                  40                  45
ggt ttt aaa aac gcc ata gcc acg ctt ggg aca gct tta acg cca tcg   192
Gly Phe Lys Asn Ala Ile Ala Thr Leu Gly Thr Ala Leu Thr Pro Ser
     50                  55                  60
cat ttg ccc ttg ctt aaa aaa ggc gat ccc gaa atc ctt ttg agc tat   240
His Leu Pro Leu Leu Lys Lys Gly Asp Pro Glu Ile Leu Leu Ser Tyr
 65                  70                  75                  80
gat ggg gat aag gca ggg cga aac gca gcc tat aaa gcg agc ttg atg   288
Asp Gly Asp Lys Ala Gly Arg Asn Ala Ala Tyr Lys Ala Ser Leu Met
                 85                  90                  95
ttg gct aaa gag caa agg agg gga ggg gtg att ttg ttt gaa aac aac   336
Leu Ala Lys Glu Gln Arg Arg Gly Gly Val Ile Leu Phe Glu Asn Asn
            100                 105                 110
ctg gat cca gcg gat atg atc gct aat ggc cag att gaa acc tta aaa   384
Leu Asp Pro Ala Asp Met Ile Ala Asn Gly Gln Ile Glu Thr Leu Lys
        115                 120                 125
aat tgg cta tcg cac ccc atg gct ttt att gag ttt gtt tta agg cgc   432
Asn Trp Leu Ser His Pro Met Ala Phe Ile Glu Phe Val Leu Arg Arg
    130                 135                 140
atg gcg gat tcc tat ctt tta gac gat cct tta gaa aaa gat aag gct   480
Met Ala Asp Ser Tyr Leu Leu Asp Asp Pro Leu Glu Lys Asp Lys Ala
145                 150                 155                 160
ctt aaa gaa atg tta ggg ttt tta aaa aac ttt tcc ttg ctt tta caa   528
Leu Lys Glu Met Leu Gly Phe Leu Lys Asn Phe Ser Leu Leu Leu Gln
                165                 170                 175
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agc gaa tac aag ccc tta atc gct acc ctt ttg caa gcg cct ttg cat   576
Ser Glu Tyr Lys Pro Leu Ile Ala Thr Leu Leu Gln Ala Pro Leu His
            180                 185                 190
gtt tta ggg att aga gag cga gtc tct ttt cag cct ttt tac ccc aaa   624
Val Leu Gly Ile Arg Glu Arg Val Ser Phe Gln Pro Phe Tyr Pro Lys
        195                 200                 205
aca gaa aaa ccc aat cgc cct caa                                   648
Thr Glu Lys Pro Asn Arg Pro Gln
    210                 215
<210> 222
<211> 216
<212> PRT
<213> Helicobacter pylori
<400> 222
Lys Tyr Ile Asn Ser Pro Gln Ser Lys Leu Phe Asp Lys Ser Ser Leu
  1               5                  10                  15
Leu Tyr Gly Tyr His Leu Ala Lys Glu His Ile Tyr Lys Gln Lys Gln
             20                  25                  30
Val Ile Val Thr Glu Gly Tyr Leu Asp Val Ile Leu Leu His Gln Ala
         35                  40                  45
Gly Phe Lys Asn Ala Ile Ala Thr Leu Gly Thr Ala Leu Thr Pro Ser
     50                  55                  60
His Leu Pro Leu Leu Lys Lys Gly Asp Pro Glu Ile Leu Leu Ser Tyr
 65                  70                  75                  80
Asp Gly Asp Lys Ala Gly Arg Asn Ala Ala Tyr Lys Ala Ser Leu Met
                 85                  90                  95
Leu Ala Lys Glu Gln Arg Arg Gly Gly Val Ile Leu Phe Glu Asn Asn
            100                 105                 110
Leu Asp Pro Ala Asp Met Ile Ala Asn Gly Gln Ile Glu Thr Leu Lys
        115                 120                 125
Asn Trp Leu Ser His Pro Met Ala Phe Ile Glu Phe Val Leu Arg Arg
    130                 135                 140
Met Ala Asp Ser Tyr Leu Leu Asp Asp Pro Leu Glu Lys Asp Lys Ala
145                 150                 155                 160
Leu Lys Glu Met Leu Gly Phe Leu Lys Asn Phe Ser Leu Leu Leu Gln
                165                 170                 175
Ser Glu Tyr Lys Pro Leu Ile Ala Thr Leu Leu Gln Ala Pro Leu His
            180                 185                 190
Val Leu Gly Ile Arg Glu Arg Val Ser Phe Gln Pro Phe Tyr Pro Lys
        195                 200                 205
Thr Glu Lys Pro Asn Arg Pro Gln
    210                 215
<210> 223
<211> 864
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(864)
<400> 223
act caa atg gct ttt gat ttt aat acg ccc ttg ttg caa gtc cag cac    48
Thr Gln Met Ala Phe Asp Phe Asn Thr Pro Leu Leu Gln Val Gln His
  1               5                  10                  15
cac cat gcc cac ttt tta gcg agc gtc tta gac gca ttg tta caa gat    96
His His Ala His Phe Leu Ala Ser Val Leu Asp Ala Leu Leu Gln Asp
             20                  25                  30
ccg cat tta aat cac ccc ttt ata ggc att gtc tgg gat ggg agt ggg   144
Pro His Leu Asn His Pro Phe Ile Gly Ile Val Trp Asp Gly Ser Gly
         35                  40                  45
gct tat gaa aat aag att tat ggg gcg gag tgt ttt gtg ggg gat ttg   192
Ala Tyr Glu Asn Lys Ile Tyr Gly Ala Glu Cys Phe Val Gly Asp Leu
```

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     50                  55                  60
gaa cgc att gaa gaa acc gcc agg ttt gaa gaa ttt tgg ctt tta ggg   240
Glu Arg Ile Glu Glu Thr Ala Arg Phe Glu Glu Phe Trp Leu Leu Gly
 65                  70                  75                  80
ggg caa aaa gcg atc aaa gag cct aga cgc ctg gtt tta gaa atc gct   288
Gly Gln Lys Ala Ile Lys Glu Pro Arg Arg Leu Val Leu Glu Ile Ala
                 85                  90                  95
tta aaa cac caa ctc aac aag ctt tta aag cgc gtt caa aag cat ttt   336
Leu Lys His Gln Leu Asn Lys Leu Leu Lys Arg Val Gln Lys His Phe
            100                 105                 110
aaa gaa gac gaa tta gaa att ttc caa caa atg cat gac aaa aaa att   384
Lys Glu Asp Glu Leu Glu Ile Phe Gln Gln Met His Asp Lys Lys Ile
        115                 120                 125
caa agc ata gcc acc aat tcc ata ggg cgt ttg ttt gat ata gta gcg   432
Gln Ser Ile Ala Thr Asn Ser Ile Gly Arg Leu Phe Asp Ile Val Ala
    130                 135                 140
ttt agt ttg gat tta aca gga acg att agc ttt gaa gca gag agc ggg   480
Phe Ser Leu Asp Leu Thr Gly Thr Ile Ser Phe Glu Ala Glu Ser Gly
145                 150                 155                 160
cag gtt tta gaa aat cta gcc tta caa agc gat gag atc gct ttt tac   528
Gln Val Leu Glu Asn Leu Ala Leu Gln Ser Asp Glu Ile Ala Phe Tyr
                165                 170                 175
cct ttt gaa atc aaa aac agc gtg gtg tgt ttg aaa gaa ttt tat caa   576
Pro Phe Glu Ile Lys Asn Ser Val Val Cys Leu Lys Glu Phe Tyr Gln
            180                 185                 190
gcg ttt gaa aag gat ttg ggc gtt tta gag cct gaa cgc atc gct aag   624
Ala Phe Glu Lys Asp Leu Gly Val Leu Glu Pro Glu Arg Ile Ala Lys
        195                 200                 205
aaa ttt ttt aac agc cta gta gaa atc att acc gct tta atc gtg cct   672
Lys Phe Phe Asn Ser Leu Val Glu Ile Ile Thr Ala Leu Ile Val Pro
    210                 215                 220
ttt aaa gag cat gtg gtg gtg tgc agt ggg ggc gtg ttt tgc aac caa   720
Phe Lys Glu His Val Val Val Cys Ser Gly Gly Val Phe Cys Asn Gln
225                 230                 235                 240
tta tta tgc gaa caa tta gcc aaa cga ttg aga ggg cta aag agg cag   768
Leu Leu Cys Glu Gln Leu Ala Lys Arg Leu Arg Gly Leu Lys Arg Gln
                245                 250                 255
tat ttt ttc cac aag cat ttc ccc cct aat gac agc agt atc cct atc   816
Tyr Phe Phe His Lys His Phe Pro Pro Asn Asp Ser Ser Ile Pro Ile
            260                 265                 270
ggt caa gcc tta atg gcg tat ttc aac cct aca atc atc aaa aaa gga   864
Gly Gln Ala Leu Met Ala Tyr Phe Asn Pro Thr Ile Ile Lys Lys Gly
        275                 280                 285
<210> 224
<211> 288
<212> PRT
<213> Helicobacter pylori
<400> 224
Thr Gln Met Ala Phe Asp Phe Asn Thr Pro Leu Leu Gln Val Gln His
  1               5                  10                  15
His His Ala His Phe Leu Ala Ser Val Leu Asp Ala Leu Leu Gln Asp
             20                  25                  30
Pro His Leu Asn His Pro Phe Ile Gly Ile Val Trp Asp Gly Ser Gly
         35                  40                  45
Ala Tyr Glu Asn Lys Ile Tyr Gly Ala Glu Cys Phe Val Gly Asp Leu
     50                  55                  60
Glu Arg Ile Glu Glu Thr Ala Arg Phe Glu Glu Phe Trp Leu Leu Gly
 65                  70                  75                  80
Gly Gln Lys Ala Ile Lys Glu Pro Arg Arg Leu Val Leu Glu Ile Ala
                 85                  90                  95
Leu Lys His Gln Leu Asn Lys Leu Leu Lys Arg Val Gln Lys His Phe
```

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            100                 105                 110
Lys Glu Asp Glu Leu Glu Ile Phe Gln Gln Met His Asp Lys Lys Ile
        115                 120                 125
Gln Ser Ile Ala Thr Asn Ser Ile Gly Arg Leu Phe Asp Ile Val Ala
    130                 135                 140
Phe Ser Leu Asp Leu Thr Gly Thr Ile Ser Phe Glu Ala Glu Ser Gly
145                 150                 155                 160
Gln Val Leu Glu Asn Leu Ala Leu Gln Ser Asp Glu Ile Ala Phe Tyr
                165                 170                 175
Pro Phe Glu Ile Lys Asn Ser Val Val Cys Leu Lys Glu Phe Tyr Gln
            180                 185                 190
Ala Phe Glu Lys Asp Leu Gly Val Leu Glu Pro Glu Arg Ile Ala Lys
        195                 200                 205
Lys Phe Phe Asn Ser Leu Val Glu Ile Ile Thr Ala Leu Ile Val Pro
    210                 215                 220
Phe Lys Glu His Val Val Val Cys Ser Gly Gly Val Phe Cys Asn Gln
225                 230                 235                 240
Leu Leu Cys Glu Gln Leu Ala Lys Arg Leu Arg Gly Leu Lys Arg Gln
                245                 250                 255
Tyr Phe Phe His Lys His Phe Pro Pro Asn Asp Ser Ser Ile Pro Ile
            260                 265                 270
Gly Gln Ala Leu Met Ala Tyr Phe Asn Pro Thr Ile Ile Lys Lys Gly
        275                 280                 285
<210> 225
<211> 159
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(159)
<400> 225
caa gga atc tta cct cct acc atc aat caa gaa atg cct gac cca gaa   48
Gln Gly Ile Leu Pro Pro Thr Ile Asn Gln Glu Met Pro Asp Pro Glu
  1               5                  10                  15
tgc gat ttg gat tat atc cct aat gcg gcc aga gaa aag cga gtg gat   96
Cys Asp Leu Asp Tyr Ile Pro Asn Ala Ala Arg Glu Lys Arg Val Asp
            20                  25                  30
gca gtg atg agt aac tca ttt ggt ttt ggt ggc act aat ggt gtt gtg   144
Ala Val Met Ser Asn Ser Phe Gly Phe Gly Gly Thr Asn Gly Val Val
        35                  40                  45
att ttc aaa aaa gcc                                              159
Ile Phe Lys Lys Ala
    50
<210> 226
<211> 53
<212> PRT
<213> Helicobacter pylori
<400> 226
Gln Gly Ile Leu Pro Pro Thr Ile Asn Gln Glu Met Pro Asp Pro Glu
  1               5                  10                  15
Cys Asp Leu Asp Tyr Ile Pro Asn Ala Ala Arg Glu Lys Arg Val Asp
            20                  25                  30
Ala Val Met Ser Asn Ser Phe Gly Phe Gly Gly Thr Asn Gly Val Val
        35                  40                  45
Ile Phe Lys Lys Ala
    50
<210> 227
<211> 1293
<212> DNA
<213> Helicobacter pylori
<220>
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<221> CDS
<222> (1)..(1293)
<400> 227

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ttt ggg aat aag cag ttg caa ctt caa atc agt cag aaa gat tct gag   48
Phe Gly Asn Lys Gln Leu Gln Leu Gln Ile Ser Gln Lys Asp Ser Glu
 1               5                  10                  15
att gcg gag tta aaa aaa gaa gtc aat ctt tat caa agc ctt tta aat   96
Ile Ala Glu Leu Lys Lys Glu Val Asn Leu Tyr Gln Ser Leu Leu Asn
            20                  25                  30
ttg tgc ttg cat gag ggt ttt gta ggt att aaa aac aat aaa gtc gtt  144
Leu Cys Leu His Glu Gly Phe Val Gly Ile Lys Asn Asn Lys Val Val
        35                  40                  45
ttt aaa agt ggg aat ctt gca agc ttg aac aat tta gaa gaa caa agc  192
Phe Lys Ser Gly Asn Leu Ala Ser Leu Asn Asn Leu Glu Glu Gln Ser
    50                  55                  60
gtt cat ttt aaa gaa aat gca gag agc gtt aat tta caa ggg gtt tct  240
Val His Phe Lys Glu Asn Ala Glu Ser Val Asn Leu Gln Gly Val Ser
65                  70                  75                  80
tat tct tta aaa agc caa aat att gat ggc gtg cag tat ttt tca ttg  288
Tyr Ser Leu Lys Ser Gln Asn Ile Asp Gly Val Gln Tyr Phe Ser Leu
                85                  90                  95
gct aaa aac aca agt tgt gtg ggg gaa tac cat aaa aat gat ttg ttt  336
Ala Lys Asn Thr Ser Cys Val Gly Glu Tyr His Lys Asn Asp Leu Phe
            100                 105                 110
aag act ttt tgc gcg agc tta aaa gaa ggc tta gag aac gcg caa gaa  384
Lys Thr Phe Cys Ala Ser Leu Lys Glu Gly Leu Glu Asn Ala Gln Glu
        115                 120                 125
agc atg cag tat ttc cat caa gaa acc ggt gct ctt tta aat gca gct  432
Ser Met Gln Tyr Phe His Gln Glu Thr Gly Ala Leu Leu Asn Ala Ala
    130                 135                 140
aaa aat ggc gaa gcg cat tct act gaa gga ttg ggg acg gtt aat aaa  480
Lys Asn Gly Glu Ala His Ser Thr Glu Gly Leu Gly Thr Val Asn Lys
145                 150                 155                 160
acg ggg caa gac att gaa tcg ctt tat gaa aag atg caa aac gcc act  528
Thr Gly Gln Asp Ile Glu Ser Leu Tyr Glu Lys Met Gln Asn Ala Thr
                165                 170                 175
tcg cta gcg gac tct ctc aac caa cgg agc aat gaa atc act caa gtc  576
Ser Leu Ala Asp Ser Leu Asn Gln Arg Ser Asn Glu Ile Thr Gln Val
            180                 185                 190
att tct ttg att gat gat att gca gaa caa acc aat cta tta gcc cta  624
Ile Ser Leu Ile Asp Asp Ile Ala Glu Gln Thr Asn Leu Leu Ala Leu
        195                 200                 205
aat gcc gct att gag gcc gcg cga gcg ggc gag cat ggg aga ggg ttt  672
Asn Ala Ala Ile Glu Ala Ala Arg Ala Gly Glu His Gly Arg Gly Phe
    210                 215                 220
gcg gtg gtg gct gat gag gtg aga aaa ctc gct gaa aaa acc caa aaa  720
Ala Val Val Ala Asp Glu Val Arg Lys Leu Ala Glu Lys Thr Gln Lys
225                 230                 235                 240
gcc act aaa gaa atc gct gtt gtc gtt aaa agc atg caa caa gaa gcg  768
Ala Thr Lys Glu Ile Ala Val Val Val Lys Ser Met Gln Gln Glu Ala
                245                 250                 255
aac gat att caa acc aat acc cac gat att aat tct att gta agc tct  816
Asn Asp Ile Gln Thr Asn Thr His Asp Ile Asn Ser Ile Val Ser Ser
            260                 265                 270
att aag ggc gat gtg gaa gag ctt aaa tcc acc gta aaa aat aac atg  864
Ile Lys Gly Asp Val Glu Glu Leu Lys Ser Thr Val Lys Asn Asn Met
        275                 280                 285
att gtt gcg caa gcg gca aaa tac acc atc tac aat atc aat aac cgg  912
Ile Val Ala Gln Ala Ala Lys Tyr Thr Ile Tyr Asn Ile Asn Asn Arg
    290                 295                 300
gtg ttt tgc ggt ttg gcc aaa ctt gat cat gtg gtc ttt aaa aac aat  960
```

```
Val Phe Cys Gly Leu Ala Lys Leu Asp His Val Val Phe Lys Asn Asn
305                 310                 315                 320
ctt tat ggc atg gtt ttt ggt ctc aat tcc ttt gat att acc agc cat   1008
Leu Tyr Gly Met Val Phe Gly Leu Asn Ser Phe Asp Ile Thr Ser His
                325                 330                 335
aag aat tgc cgt tta ggc aaa tgg tat tat gag ggc gcg ggc aaa gag   1056
Lys Asn Cys Arg Leu Gly Lys Trp Tyr Tyr Glu Gly Ala Gly Lys Glu
            340                 345                 350
aat ttt tcc aac act tca ggc tat aga gct tta gaa agc cac cat gca   1104
Asn Phe Ser Asn Thr Ser Gly Tyr Arg Ala Leu Glu Ser His His Ala
        355                 360                 365
agc gtg cat gct gaa gct aat gat ttg gtt aaa gcc gtt caa gaa gac   1152
Ser Val His Ala Glu Ala Asn Asp Leu Val Lys Ala Val Gln Glu Asp
    370                 375                 380
cac att acc gat tca aaa tac cta gag cat aaa gtg cat tta atg gaa   1200
His Ile Thr Asp Ser Lys Tyr Leu Glu His Lys Val His Leu Met Glu
385                 390                 395                 400
gat agt gct aaa cat gtt aga gaa aat att gat aag atg ttt tac gaa   1248
Asp Ser Ala Lys His Val Arg Glu Asn Ile Asp Lys Met Phe Tyr Glu
                405                 410                 415
aaa caa gat gaa ctc aat aaa atc att gaa aaa att caa aaa ggc       1293
Lys Gln Asp Glu Leu Asn Lys Ile Ile Glu Lys Ile Gln Lys Gly
            420                 425                 430
```

<210> 228
<211> 431
<212> PRT
<213> Helicobacter pylori
<400> 228

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Phe Gly Asn Lys Gln Leu Gln Leu Gln Ile Ser Gln Lys Asp Ser Glu
  1               5                  10                  15
Ile Ala Glu Leu Lys Lys Glu Val Asn Leu Tyr Gln Ser Leu Leu Asn
            20                  25                  30
Leu Cys Leu His Glu Gly Phe Val Gly Ile Lys Asn Asn Lys Val Val
        35                  40                  45
Phe Lys Ser Gly Asn Leu Ala Ser Leu Asn Asn Leu Glu Glu Gln Ser
    50                  55                  60
Val His Phe Lys Glu Asn Ala Glu Ser Val Asn Leu Gln Gly Val Ser
65                  70                  75                  80
Tyr Ser Leu Lys Ser Gln Asn Ile Asp Gly Val Gln Tyr Phe Ser Leu
                85                  90                  95
Ala Lys Asn Thr Ser Cys Val Gly Glu Tyr His Lys Asn Asp Leu Phe
            100                 105                 110
Lys Thr Phe Cys Ala Ser Leu Lys Glu Gly Leu Glu Asn Ala Gln Glu
        115                 120                 125
Ser Met Gln Tyr Phe His Gln Glu Thr Gly Ala Leu Leu Asn Ala Ala
    130                 135                 140
Lys Asn Gly Glu Ala His Ser Thr Glu Gly Leu Gly Thr Val Asn Lys
145                 150                 155                 160
Thr Gly Gln Asp Ile Glu Ser Leu Tyr Glu Lys Met Gln Asn Ala Thr
                165                 170                 175
Ser Leu Ala Asp Ser Leu Asn Gln Arg Ser Asn Glu Ile Thr Gln Val
            180                 185                 190
Ile Ser Leu Ile Asp Asp Ile Ala Glu Gln Thr Asn Leu Leu Ala Leu
        195                 200                 205
Asn Ala Ala Ile Glu Ala Ala Arg Ala Gly Glu His Gly Arg Gly Phe
    210                 215                 220
Ala Val Val Ala Asp Glu Val Arg Lys Leu Ala Glu Lys Thr Gln Lys
225                 230                 235                 240
Ala Thr Lys Glu Ile Ala Val Val Val Lys Ser Met Gln Gln Glu Ala
                245                 250                 255
Asn Asp Ile Gln Thr Asn Thr His Asp Ile Asn Ser Ile Val Ser Ser
```

```
            260                 265                 270
Ile Lys Gly Asp Val Glu Glu Leu Lys Ser Thr Val Lys Asn Asn Met
        275                 280                 285
Ile Val Ala Gln Ala Ala Lys Tyr Thr Ile Tyr Asn Ile Asn Asn Arg
    290                 295                 300
Val Phe Cys Gly Leu Ala Lys Leu Asp His Val Val Phe Lys Asn Asn
305                 310                 315                 320
Leu Tyr Gly Met Val Phe Gly Leu Asn Ser Phe Asp Ile Thr Ser His
                325                 330                 335
Lys Asn Cys Arg Leu Gly Lys Trp Tyr Tyr Glu Gly Ala Gly Lys Glu
            340                 345                 350
Asn Phe Ser Asn Thr Ser Gly Tyr Arg Ala Leu Glu Ser His His Ala
        355                 360                 365
Ser Val His Ala Glu Ala Asn Asp Leu Val Lys Ala Val Gln Glu Asp
    370                 375                 380
His Ile Thr Asp Ser Lys Tyr Leu Glu His Lys Val His Leu Met Glu
385                 390                 395                 400
Asp Ser Ala Lys His Val Arg Glu Asn Ile Asp Lys Met Phe Tyr Glu
                405                 410                 415
Lys Gln Asp Glu Leu Asn Lys Ile Ile Glu Lys Ile Gln Lys Gly
            420                 425                 430
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<210> 229
<211> 286
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(285)
<400> 229

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gat ttg aat gcg att tta gaa gat ctc aac agc aaa cag cta ttg cca   48
Asp Leu Asn Ala Ile Leu Glu Asp Leu Asn Ser Lys Gln Leu Leu Pro
  1               5                  10                  15
gaa tac gct tac aag gtt tat ggc gca gtg gtg agt caa aat aaa gac   96
Glu Tyr Ala Tyr Lys Val Tyr Gly Ala Val Val Ser Gln Asn Lys Asp
             20                  25                  30
ggc gtg tgg gtc ggc gat gaa gcc aaa acg aaa gcc aga aga aaa gaa   144
Gly Val Trp Val Gly Asp Glu Ala Lys Thr Lys Ala Arg Arg Lys Glu
         35                  40                  45
att ctt gaa aac aga aag gct aga tcc ata ccg gta aaa caa tgg atg   192
Ile Leu Glu Asn Arg Lys Ala Arg Ser Ile Pro Val Lys Gln Trp Met
     50                  55                  60
gag caa gaa aga aac gct atc ctt gaa aaa gag gct tcc aaa cag gtt   240
Glu Gln Glu Arg Asn Ala Ile Leu Glu Lys Glu Ala Ser Lys Gln Val
 65                  70                  75                  80
aag cac atg tat gcg act agc ttt gat ctc tcg cct aag ttt ttg a     286
Lys His Met Tyr Ala Thr Ser Phe Asp Leu Ser Pro Lys Phe Leu
                85                  90                  95
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<210> 230
<211> 95
<212> PRT
<213> Helicobacter pylori
<400> 230

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Asp Leu Asn Ala Ile Leu Glu Asp Leu Asn Ser Lys Gln Leu Leu Pro
  1               5                  10                  15
Glu Tyr Ala Tyr Lys Val Tyr Gly Ala Val Val Ser Gln Asn Lys Asp
             20                  25                  30
Gly Val Trp Val Gly Asp Glu Ala Lys Thr Lys Ala Arg Arg Lys Glu
         35                  40                  45
Ile Leu Glu Asn Arg Lys Ala Arg Ser Ile Pro Val Lys Gln Trp Met
     50                  55                  60
Glu Gln Glu Arg Asn Ala Ile Leu Glu Lys Glu Ala Ser Lys Gln Val
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65 70 75 80
Lys His Met Tyr Ala Thr Ser Phe Asp Leu Ser Pro Lys Phe Leu
85 90 95

<210> 231
<211> 163
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(162)
<400> 231
aga cgc aat caa aaa agc gca tca aag ttt atc aac tat ccc tct aag 48
Arg Arg Asn Gln Lys Ser Ala Ser Lys Phe Ile Asn Tyr Pro Ser Lys
1 5 10 15
ttc ttc act cta tgc tat aat ctc tgt ttt aaa aca tta tgg aat gtt 96
Phe Phe Thr Leu Cys Tyr Asn Leu Cys Phe Lys Thr Leu Trp Asn Val
20 25 30
aga aga tat tca gca aaa ccc ttc caa acc aac caa tct aaa gaa aga 144
Arg Arg Tyr Ser Ala Lys Pro Phe Gln Thr Asn Gln Ser Lys Glu Arg
35 40 45
aac cat tca agg aac gca t 163
Asn His Ser Arg Asn Ala
50

<210> 232
<211> 54
<212> PRT
<213> Helicobacter pylori
<400> 232
Arg Arg Asn Gln Lys Ser Ala Ser Lys Phe Ile Asn Tyr Pro Ser Lys
1 5 10 15
Phe Phe Thr Leu Cys Tyr Asn Leu Cys Phe Lys Thr Leu Trp Asn Val
20 25 30
Arg Arg Tyr Ser Ala Lys Pro Phe Gln Thr Asn Gln Ser Lys Glu Arg
35 40 45
Asn His Ser Arg Asn Ala
50

<210> 233
<211> 222
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(222)
<400> 233
gac gat cgc tcg ttt ttt atc act gat tct cgc tac act caa gaa gct 48
Asp Asp Arg Ser Phe Phe Ile Thr Asp Ser Arg Tyr Thr Gln Glu Ala
1 5 10 15
aaa gaa agc gtt cag cct aaa aat ggc gtt tta gcg gaa gtg gta gaa 96
Lys Glu Ser Val Gln Pro Lys Asn Gly Val Leu Ala Glu Val Val Glu
20 25 30
tct agc gat tta gtg caa agc gcg att gat ttg att gtt aaa agt tcg 144
Ser Ser Asp Leu Val Gln Ser Ala Ile Asp Leu Ile Val Lys Ser Ser
35 40 45
gtt aaa aaa ctc ttt ttt gac ccc aat caa gtg aat tta caa acc tac 192
Val Lys Lys Leu Phe Phe Asp Pro Asn Gln Val Asn Leu Gln Thr Tyr
50 55 60
aag cgt tta aat tca gcg ctt ggg gat aag 222
Lys Arg Leu Asn Ser Ala Leu Gly Asp Lys
65 70

<210> 234
<211> 74

<212> PRT
<213> Helicobacter pylori
<400> 234
Asp Asp Arg Ser Phe Phe Ile Thr Asp Ser Arg Tyr Thr Gln Glu Ala
1 5 10 15
Lys Glu Ser Val Gln Pro Lys Asn Gly Val Leu Ala Glu Val Val Glu
20 25 30
Ser Ser Asp Leu Val Gln Ser Ala Ile Asp Leu Ile Val Lys Ser Ser
35 40 45
Val Lys Lys Leu Phe Phe Asp Pro Asn Gln Val Asn Leu Gln Thr Tyr
50 55 60
Lys Arg Leu Asn Ser Ala Leu Gly Asp Lys
65 70
<210> 235
<211> 108
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(108)
<400> 235
ctt ggc tac aac atg gct tta atg gcg atg gtc aat att tta gcc gaa 48
Leu Gly Tyr Asn Met Ala Leu Met Ala Met Val Asn Ile Leu Ala Glu
1 5 10 15
atg aaa gcg ttc caa gaa gcc caa aaa aac aac cct aat aac ccc att 96
Met Lys Ala Phe Gln Glu Ala Gln Lys Asn Asn Pro Asn Asn Pro Ile
20 25 30
aac aat caa aaa 108
Asn Asn Gln Lys
35
<210> 236
<211> 36
<212> PRT
<213> Helicobacter pylori
<400> 236
Leu Gly Tyr Asn Met Ala Leu Met Ala Met Val Asn Ile Leu Ala Glu
1 5 10 15
Met Lys Ala Phe Gln Glu Ala Gln Lys Asn Asn Pro Asn Asn Pro Ile
20 25 30
Asn Asn Gln Lys
35
<210> 237
<211> 381
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(381)
<400> 237
tct aaa gag agc ttg atg cat gcc att aat tca att aga gtg ggc atg 48
Ser Lys Glu Ser Leu Met His Ala Ile Asn Ser Ile Arg Val Gly Met
1 5 10 15
cat ttt aaa gag ttg agt cag att tta gag agc act att aca gaa agg 96
His Phe Lys Glu Leu Ser Gln Ile Leu Glu Ser Thr Ile Thr Glu Arg
20 25 30
ggc ttt gtg cct ttg aaa gga ttt tgc ggg cat ggc att ggt aaa aaa 144
Gly Phe Val Pro Leu Lys Gly Phe Cys Gly His Gly Ile Gly Lys Lys
35 40 45
ccc cat gaa gag cca gag atc ccc aac tac cta gaa aaa ggc gtc aaa 192
Pro His Glu Glu Pro Glu Ile Pro Asn Tyr Leu Glu Lys Gly Val Lys
50 55 60

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cct aat agc ggc cct aaa atc aaa gag ggc atg gta ttt tgc tta gag   240
Pro Asn Ser Gly Pro Lys Ile Lys Glu Gly Met Val Phe Cys Leu Glu
 65                  70                  75                  80
cct atg gtg tgt caa aaa cag ggc gag cct aaa ata cta gcg gat aag   288
Pro Met Val Cys Gln Lys Gln Gly Glu Pro Lys Ile Leu Ala Asp Lys
                85                  90                  95
tgg agc gtg gtt tca gtg gat ggg ctt aac aca agc cac cat gag cat   336
Trp Ser Val Val Ser Val Asp Gly Leu Asn Thr Ser His His Glu His
            100                 105                 110
act atc gcc ata gtt ggc aat aaa gca gtg att ctt acg gag cgt       381
Thr Ile Ala Ile Val Gly Asn Lys Ala Val Ile Leu Thr Glu Arg
        115                 120                 125
<210> 238
<211> 127
<212> PRT
<213> Helicobacter pylori
<400> 238
Ser Lys Glu Ser Leu Met His Ala Ile Asn Ser Ile Arg Val Gly Met
  1               5                  10                  15
His Phe Lys Glu Leu Ser Gln Ile Leu Glu Ser Thr Ile Thr Glu Arg
            20                  25                  30
Gly Phe Val Pro Leu Lys Gly Phe Cys Gly His Gly Ile Gly Lys Lys
        35                  40                  45
Pro His Glu Glu Pro Glu Ile Pro Asn Tyr Leu Glu Lys Gly Val Lys
    50                  55                  60
Pro Asn Ser Gly Pro Lys Ile Lys Glu Gly Met Val Phe Cys Leu Glu
 65                  70                  75                  80
Pro Met Val Cys Gln Lys Gln Gly Glu Pro Lys Ile Leu Ala Asp Lys
                85                  90                  95
Trp Ser Val Val Ser Val Asp Gly Leu Asn Thr Ser His His Glu His
            100                 105                 110
Thr Ile Ala Ile Val Gly Asn Lys Ala Val Ile Leu Thr Glu Arg
        115                 120                 125
<210> 239
<211> 242
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(240)
<400> 239
cag ctc agc ggt ggg caa aaa caa cga gtg gcg atc gct agg agt tta    48
Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Ala Ile Ala Arg Ser Leu
  1               5                  10                  15
gcg aat tgc cct gat tta ttg ctt tgc gat gaa gcc aca tcc gcg cta    96
Ala Asn Cys Pro Asp Leu Leu Leu Cys Asp Glu Ala Thr Ser Ala Leu
            20                  25                  30
gat tct aaa acc acg cat tct att tta acg ctt tta agc ggc att caa   144
Asp Ser Lys Thr Thr His Ser Ile Leu Thr Leu Leu Ser Gly Ile Gln
        35                  40                  45
aaa aag ctt gat ttg agc atc gtt ttc atc acg cat gaa att gaa gtg   192
Lys Lys Leu Asp Leu Ser Ile Val Phe Ile Thr His Glu Ile Glu Val
    50                  55                  60
gtt aaa gaa ttg tgc aat caa atg tgc gtg atc agc agc ggc gaa atc   240
Val Lys Glu Leu Cys Asn Gln Met Cys Val Ile Ser Ser Gly Glu Ile
 65                  70                  75                  80
gt                                                               242
<210> 240
<211> 80
<212> PRT
<213> Helicobacter pylori
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<400> 240
Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Ala Ile Ala Arg Ser Leu
1 5 10 15
Ala Asn Cys Pro Asp Leu Leu Leu Cys Asp Glu Ala Thr Ser Ala Leu
20 25 30
Asp Ser Lys Thr Thr His Ser Ile Leu Thr Leu Leu Ser Gly Ile Gln
35 40 45
Lys Lys Leu Asp Leu Ser Ile Val Phe Ile Thr His Glu Ile Glu Val
50 55 60
Val Lys Glu Leu Cys Asn Gln Met Cys Val Ile Ser Ser Gly Glu Ile
65 70 75 80
<210> 241
<211> 471
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(471)
<400> 241
tat ggc aag caa agc ttg agt tct ttt gcc aat aat ttt gtg cct gga 48
Tyr Gly Lys Gln Ser Leu Ser Ser Phe Ala Asn Asn Phe Val Pro Gly
1 5 10 15
ggc ttg aat caa gcc ctt gat aaa ata ggc tct agc tct gat gcc aaa 96
Gly Leu Asn Gln Ala Leu Asp Lys Ile Gly Ser Ser Ser Asp Ala Lys
20 25 30
gac tta cag aac ttc ttg gat aaa acg act ttt ggg gat att tta aat 144
Asp Leu Gln Asn Phe Leu Asp Lys Thr Thr Phe Gly Asp Ile Leu Asn
35 40 45
caa atg att gaa caa gcc ccc tta atc aat aaa ctc att tct tgg ctg 192
Gln Met Ile Glu Gln Ala Pro Leu Ile Asn Lys Leu Ile Ser Trp Leu
50 55 60
ggt ccg cag gat ttg agc gtt tta gtg aat atc gct tta aat agc atc 240
Gly Pro Gln Asp Leu Ser Val Leu Val Asn Ile Ala Leu Asn Ser Ile
65 70 75 80
act aac cct agt aaa gag ctg act agc acc att tct agc ata ggt gaa 288
Thr Asn Pro Ser Lys Glu Leu Thr Ser Thr Ile Ser Ser Ile Gly Glu
85 90 95
aaa gcg tta aat gac tta tta ggc gat ggc gta gtg aat aaa atc atg 336
Lys Ala Leu Asn Asp Leu Leu Gly Asp Gly Val Val Asn Lys Ile Met
100 105 110
agc aat caa gtc tta ggg caa atg atc aat aaa atc att gct gat aag 384
Ser Asn Gln Val Leu Gly Gln Met Ile Asn Lys Ile Ile Ala Asp Lys
115 120 125
ggc ttt gga ggc gtt tat cag caa ggt tta ggc tcc ata ctg cct caa 432
Gly Phe Gly Gly Val Tyr Gln Gln Gly Leu Gly Ser Ile Leu Pro Gln
130 135 140
tct tta caa gat gaa ttg aag aaa ttg ggc atg ggc tct 471
Ser Leu Gln Asp Glu Leu Lys Lys Leu Gly Met Gly Ser
145 150 155
<210> 242
<211> 157
<212> PRT
<213> Helicobacter pylori
<400> 242
Tyr Gly Lys Gln Ser Leu Ser Ser Phe Ala Asn Asn Phe Val Pro Gly
1 5 10 15
Gly Leu Asn Gln Ala Leu Asp Lys Ile Gly Ser Ser Ser Asp Ala Lys
20 25 30
Asp Leu Gln Asn Phe Leu Asp Lys Thr Thr Phe Gly Asp Ile Leu Asn
35 40 45
Gln Met Ile Glu Gln Ala Pro Leu Ile Asn Lys Leu Ile Ser Trp Leu

```
     50                  55                  60
Gly Pro Gln Asp Leu Ser Val Leu Val Asn Ile Ala Leu Asn Ser Ile
 65                  70                  75                  80
Thr Asn Pro Ser Lys Glu Leu Thr Ser Thr Ile Ser Ser Ile Gly Glu
                85                  90                  95
Lys Ala Leu Asn Asp Leu Leu Gly Asp Gly Val Val Asn Lys Ile Met
            100                 105                 110
Ser Asn Gln Val Leu Gly Gln Met Ile Asn Lys Ile Ile Ala Asp Lys
        115                 120                 125
Gly Phe Gly Gly Val Tyr Gln Gln Gly Leu Gly Ser Ile Leu Pro Gln
    130                 135                 140
Ser Leu Gln Asp Glu Leu Lys Lys Leu Gly Met Gly Ser
145                 150                 155
<210> 243
<211> 278
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(276)
<400> 243
ggg aat atc acc gtt gat ggg cct tta aga gtg aat aat caa gtg ggt   48
Gly Asn Ile Thr Val Asp Gly Pro Leu Arg Val Asn Asn Gln Val Gly
  1               5                  10                  15
ggt tat gct ttg gca gga tca agc gcg aat ttt gag ttt aag gct ggt   96
Gly Tyr Ala Leu Ala Gly Ser Ser Ala Asn Phe Glu Phe Lys Ala Gly
            20                  25                  30
acg gat acc aaa aac ggc aca gcc act ttt aat aac gat att agt ttg   144
Thr Asp Thr Lys Asn Gly Thr Ala Thr Phe Asn Asn Asp Ile Ser Leu
        35                  40                  45
gga aga ttt gtg aat tta aaa gtg gat gct cat aca gct aat ttt aaa   192
Gly Arg Phe Val Asn Leu Lys Val Asp Ala His Thr Ala Asn Phe Lys
    50                  55                  60
ggt att gat act ggt aat ggt ggt ttc aac acc tta gat ttt agt ggc   240
Gly Ile Asp Thr Gly Asn Gly Gly Phe Asn Thr Leu Asp Phe Ser Gly
65                  70                  75                  80
gtt aca ggt aag gtc aat atc aac aag ctc att acg gc                278
Val Thr Gly Lys Val Asn Ile Asn Lys Leu Ile Thr
                85                  90
<210> 244
<211> 92
<212> PRT
<213> Helicobacter pylori
<400> 244
Gly Asn Ile Thr Val Asp Gly Pro Leu Arg Val Asn Asn Gln Val Gly
  1               5                  10                  15
Gly Tyr Ala Leu Ala Gly Ser Ser Ala Asn Phe Glu Phe Lys Ala Gly
            20                  25                  30
Thr Asp Thr Lys Asn Gly Thr Ala Thr Phe Asn Asn Asp Ile Ser Leu
        35                  40                  45
Gly Arg Phe Val Asn Leu Lys Val Asp Ala His Thr Ala Asn Phe Lys
    50                  55                  60
Gly Ile Asp Thr Gly Asn Gly Gly Phe Asn Thr Leu Asp Phe Ser Gly
65                  70                  75                  80
Val Thr Gly Lys Val Asn Ile Asn Lys Leu Ile Thr
                85                  90
<210> 245
<211> 901
<212> DNA
<213> Helicobacter pylori
<220>
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<221> CDS
<222> (1)..(900)
<400> 245

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aat ggc gcg agt ggt aca ggc agt ggg aat ggc acc agt caa atc aac   48
Asn Gly Ala Ser Gly Thr Gly Ser Gly Asn Gly Thr Ser Gln Ile Asn
 1               5                  10                  15
aca gcc tac cag atg ctc aca gac gcc agc gat ggg aaa tta ggg act   96
Thr Ala Tyr Gln Met Leu Thr Asp Ala Ser Asp Gly Lys Leu Gly Thr
            20                  25                  30
tat agt agt agt agt ggc agt aat aac ggc tat acg cca tgc aat agc  144
Tyr Ser Ser Ser Ser Gly Ser Asn Asn Gly Tyr Thr Pro Cys Asn Ser
        35                  40                  45
acc aat ggg agc aat aaa acg agt ggg aac aat tgt tat gaa ccc aac  192
Thr Asn Gly Ser Asn Lys Thr Ser Gly Asn Asn Cys Tyr Glu Pro Asn
    50                  55                  60
aaa caa caa aac gcc acc acc gca acc gcc aca acc gac agc aat tta  240
Lys Gln Gln Asn Ala Thr Thr Ala Thr Ala Thr Thr Asp Ser Asn Leu
65                  70                  75                  80
caa aaa gtc tat aat gac gcc caa aaa ata gcc aac att atc gcc agc  288
Gln Lys Val Tyr Asn Asp Ala Gln Lys Ile Ala Asn Ile Ile Ala Ser
                85                  90                  95
tct ggg aac aat aaa ggc gtt gaa aac ggc tta aaa caa ttc ttt gaa  336
Ser Gly Asn Asn Lys Gly Val Glu Asn Gly Leu Lys Gln Phe Phe Glu
            100                 105                 110
gcg tta aaa aat aat agc agc agt ctc agt aat tta tgt ggt aat ggt  384
Ala Leu Lys Asn Asn Ser Ser Ser Leu Ser Asn Leu Cys Gly Asn Gly
        115                 120                 125
agt agc ggt agt agt ggc act act tgc tcc ggt tgg ctt atc aac ctt  432
Ser Ser Gly Ser Ser Gly Thr Thr Cys Ser Gly Trp Leu Ile Asn Leu
    130                 135                 140
tta ggg gca atc ccc acc aat gga gtg agc gat acg aat aat tta att  480
Leu Gly Ala Ile Pro Thr Asn Gly Val Ser Asp Thr Asn Asn Leu Ile
145                 150                 155                 160
aat ctg ctc act gaa ttc att aaa acc gcc ggg ttt atc caa aat aat  528
Asn Leu Leu Thr Glu Phe Ile Lys Thr Ala Gly Phe Ile Gln Asn Asn
                165                 170                 175
gat agt agt gta tct act agt ctt aca agc gct ttt caa gcc att acg  576
Asp Ser Ser Val Ser Thr Ser Leu Thr Ser Ala Phe Gln Ala Ile Thr
            180                 185                 190
agc gct att tct caa ggg ttt caa gcc tta caa aac gat att agc cct  624
Ser Ala Ile Ser Gln Gly Phe Gln Ala Leu Gln Asn Asp Ile Ser Pro
        195                 200                 205
aat gcg att tta acc ttg ctc caa gag att act tct aac acc acc acc  672
Asn Ala Ile Leu Thr Leu Leu Gln Glu Ile Thr Ser Asn Thr Thr Thr
    210                 215                 220
att cag tca ttc tcg caa acc tta cgg cag ctt tta ggg gat aaa aca  720
Ile Gln Ser Phe Ser Gln Thr Leu Arg Gln Leu Leu Gly Asp Lys Thr
225                 230                 235                 240
ttc ttt atg gcg caa caa aag ctc att gat gcg atg att aac gcc aga  768
Phe Phe Met Ala Gln Gln Lys Leu Ile Asp Ala Met Ile Asn Ala Arg
                245                 250                 255
aat cag gtt caa aac gcg caa aat caa gcc aat aac tac ggc tct caa  816
Asn Gln Val Gln Asn Ala Gln Asn Gln Ala Asn Asn Tyr Gly Ser Gln
            260                 265                 270
ccc gtt tta agc cag tat gcg gcc gct aaa agc acc caa cat ggc atg  864
Pro Val Leu Ser Gln Tyr Ala Ala Ala Lys Ser Thr Gln His Gly Met
        275                 280                 285
agc aat ggt tta ggg gtt ggt ttg ggc tat aaa tac t                901
Ser Asn Gly Leu Gly Val Gly Leu Gly Tyr Lys Tyr
    290                 295                 300
```

<210> 246

<211> 300
<212> PRT
<213> Helicobacter pylori
<400> 246

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Asn Gly Ala Ser Gly Thr Gly Ser Gly Asn Gly Thr Ser Gln Ile Asn
 1               5                  10                  15
Thr Ala Tyr Gln Met Leu Thr Asp Ala Ser Asp Gly Lys Leu Gly Thr
            20                  25                  30
Tyr Ser Ser Ser Ser Gly Ser Asn Asn Gly Tyr Thr Pro Cys Asn Ser
        35                  40                  45
Thr Asn Gly Ser Asn Lys Thr Ser Gly Asn Asn Cys Tyr Glu Pro Asn
    50                  55                  60
Lys Gln Gln Asn Ala Thr Thr Ala Thr Ala Thr Thr Asp Ser Asn Leu
65                  70                  75                  80
Gln Lys Val Tyr Asn Asp Ala Gln Lys Ile Ala Asn Ile Ile Ala Ser
                85                  90                  95
Ser Gly Asn Asn Lys Gly Val Glu Asn Gly Leu Lys Gln Phe Phe Glu
            100                 105                 110
Ala Leu Lys Asn Asn Ser Ser Ser Leu Ser Asn Leu Cys Gly Asn Gly
        115                 120                 125
Ser Ser Gly Ser Ser Gly Thr Thr Cys Ser Gly Trp Leu Ile Asn Leu
    130                 135                 140
Leu Gly Ala Ile Pro Thr Asn Gly Val Ser Asp Thr Asn Asn Leu Ile
145                 150                 155                 160
Asn Leu Leu Thr Glu Phe Ile Lys Thr Ala Gly Phe Ile Gln Asn Asn
                165                 170                 175
Asp Ser Ser Val Ser Thr Ser Leu Thr Ser Ala Phe Gln Ala Ile Thr
            180                 185                 190
Ser Ala Ile Ser Gln Gly Phe Gln Ala Leu Gln Asn Asp Ile Ser Pro
        195                 200                 205
Asn Ala Ile Leu Thr Leu Leu Gln Glu Ile Thr Ser Asn Thr Thr Thr
    210                 215                 220
Ile Gln Ser Phe Ser Gln Thr Leu Arg Gln Leu Leu Gly Asp Lys Thr
225                 230                 235                 240
Phe Phe Met Ala Gln Gln Lys Leu Ile Asp Ala Met Ile Asn Ala Arg
                245                 250                 255
Asn Gln Val Gln Asn Ala Gln Asn Gln Ala Asn Asn Tyr Gly Ser Gln
            260                 265                 270
Pro Val Leu Ser Gln Tyr Ala Ala Ala Lys Ser Thr Gln His Gly Met
        275                 280                 285
Ser Asn Gly Leu Gly Val Gly Leu Gly Tyr Lys Tyr
    290                 295                 300
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<210> 247
<211> 147
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(147)
<400> 247

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caa tac gac ttt aag gcg atg ttt act ccc ttg atc atg caa gcg cag   48
Gln Tyr Asp Phe Lys Ala Met Phe Thr Pro Leu Ile Met Gln Ala Gln
 1               5                  10                  15
ttg agc tta aga aac att gat aat ttt gtg gaa aaa ggc tct gct ttg   96
Leu Ser Leu Arg Asn Ile Asp Asn Phe Val Glu Lys Gly Ser Ala Leu
            20                  25                  30
ata gat aaa ttt gac gct aac ccc tat aaa acg att ttt gga gaa agg   144
Ile Asp Lys Phe Asp Ala Asn Pro Tyr Lys Thr Ile Phe Gly Glu Arg
        35                  40                  45
aaa                                                               147
Lys
```

<210> 248
<211> 49
<212> PRT
<213> Helicobacter pylori
<400> 248
Gln Tyr Asp Phe Lys Ala Met Phe Thr Pro Leu Ile Met Gln Ala Gln
1 5 10 15
Leu Ser Leu Arg Asn Ile Asp Asn Phe Val Glu Lys Gly Ser Ala Leu
20 25 30
Ile Asp Lys Phe Asp Ala Asn Pro Tyr Lys Thr Ile Phe Gly Glu Arg
35 40 45
Lys
<210> 249
<211> 249
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(249)
<400> 249
tcc aag ctg gat ttg aaa gac att tat gcg ttt tta aaa aat tta gac 48
Ser Lys Leu Asp Leu Lys Asp Ile Tyr Ala Phe Leu Lys Asn Leu Asp
1 5 10 15
aaa gaa aat ttt gat tcc aga gaa aat cag agg gaa agg att gaa agc 96
Lys Glu Asn Phe Asp Ser Arg Glu Asn Gln Arg Glu Arg Ile Glu Ser
20 25 30
ctg tta gag agc gtt aac agg cat aag atc ccc tta aac gag caa gaa 144
Leu Leu Glu Ser Val Asn Arg His Lys Ile Pro Leu Asn Glu Gln Glu
35 40 45
ttg caa gcc ttt gat tta gcg atc aag gct aac agc tct tat tac aag 192
Leu Gln Ala Phe Asp Leu Ala Ile Lys Ala Asn Ser Ser Tyr Tyr Lys
50 55 60
ctc agc tat aat ctt tta ccc ctg ctt tta agc ctt tta tcc aaa aag 240
Leu Ser Tyr Asn Leu Leu Pro Leu Leu Leu Ser Leu Leu Ser Lys Lys
65 70 75 80
aaa acg cca 249
Lys Thr Pro
<210> 250
<211> 83
<212> PRT
<213> Helicobacter pylori
<400> 250
Ser Lys Leu Asp Leu Lys Asp Ile Tyr Ala Phe Leu Lys Asn Leu Asp
1 5 10 15
Lys Glu Asn Phe Asp Ser Arg Glu Asn Gln Arg Glu Arg Ile Glu Ser
20 25 30
Leu Leu Glu Ser Val Asn Arg His Lys Ile Pro Leu Asn Glu Gln Glu
35 40 45
Leu Gln Ala Phe Asp Leu Ala Ile Lys Ala Asn Ser Ser Tyr Tyr Lys
50 55 60
Leu Ser Tyr Asn Leu Leu Pro Leu Leu Leu Ser Leu Leu Ser Lys Lys
65 70 75 80
Lys Thr Pro
<210> 251
<211> 618
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(618)
<400> 251

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gag ttt aga agt ttt ata gac aag cat tat aac cac tct ttt gag ccg   48
Glu Phe Arg Ser Phe Ile Asp Lys His Tyr Asn His Ser Phe Glu Pro
 1               5                  10                  15
cta gag gtt tta ggc tat att tat gcg tta ttg tat tcc cca aac tac   96
Leu Glu Val Leu Gly Tyr Ile Tyr Ala Leu Leu Tyr Ser Pro Asn Tyr
            20                  25                  30
cgc aag cgt tat gaa gac ttc ctt aaa aac gat tac cct aaa atc ctt   144
Arg Lys Arg Tyr Glu Asp Phe Leu Lys Asn Asp Tyr Pro Lys Ile Leu
        35                  40                  45
ttc aca aac aat aaa gat ttg ttt agg gct tta agc ctt tta ggg att   192
Phe Thr Asn Asn Lys Asp Leu Phe Arg Ala Leu Ser Leu Leu Gly Ile
    50                  55                  60
gaa cta atc ggc ttg cat gtc tta aac caa gaa agc ctg aat tac agc   240
Glu Leu Ile Gly Leu His Val Leu Asn Gln Glu Ser Leu Asn Tyr Ser
65                  70                  75                  80
ttt gga aaa tta aaa gac gcc acc ata ggc gaa tcc tgc tat aaa gaa   288
Phe Gly Lys Leu Lys Asp Ala Thr Ile Gly Glu Ser Cys Tyr Lys Glu
                85                  90                  95
gag cat aac ccc atc atc aaa aaa ccc tct cat aac gag cca gac caa   336
Glu His Asn Pro Ile Ile Lys Lys Pro Ser His Asn Glu Pro Asp Gln
            100                 105                 110
cgg ctt tat atc aac cat agc gct tat ttt agg ggg gtg agt caa gaa   384
Arg Leu Tyr Ile Asn His Ser Ala Tyr Phe Arg Gly Val Ser Gln Glu
        115                 120                 125
att tat gat tat aga ata ggg ggg tat ggc gtt tta gac aaa tat tta   432
Ile Tyr Asp Tyr Arg Ile Gly Gly Tyr Gly Val Leu Asp Lys Tyr Leu
    130                 135                 140
aaa agc cat aaa aac gag cct tgc gac ttt gat cat gta act aat atc   480
Lys Ser His Lys Asn Glu Pro Cys Asp Phe Asp His Val Thr Asn Ile
145                 150                 155                 160
att aaa gtc atc gca cgc acg att gaa atc caa aaa acg ctt gga ttt   528
Ile Lys Val Ile Ala Arg Thr Ile Glu Ile Gln Lys Thr Leu Gly Phe
                165                 170                 175
tta acg agc gat ttg ccc cat tta aaa ggg aat gac agc aaa gcc tta   576
Leu Thr Ser Asp Leu Pro His Leu Lys Gly Asn Asp Ser Lys Ala Leu
            180                 185                 190
atg caa gaa atc ttg caa aat cca ccc ccc ccc ccc ccc att           618
Met Gln Glu Ile Leu Gln Asn Pro Pro Pro Pro Pro Pro Ile
        195                 200                 205
<210> 252
<211> 206
<212> PRT
<213> Helicobacter pylori
<400> 252
Glu Phe Arg Ser Phe Ile Asp Lys His Tyr Asn His Ser Phe Glu Pro
 1               5                  10                  15
Leu Glu Val Leu Gly Tyr Ile Tyr Ala Leu Leu Tyr Ser Pro Asn Tyr
            20                  25                  30
Arg Lys Arg Tyr Glu Asp Phe Leu Lys Asn Asp Tyr Pro Lys Ile Leu
        35                  40                  45
Phe Thr Asn Asn Lys Asp Leu Phe Arg Ala Leu Ser Leu Leu Gly Ile
    50                  55                  60
Glu Leu Ile Gly Leu His Val Leu Asn Gln Glu Ser Leu Asn Tyr Ser
65                  70                  75                  80
Phe Gly Lys Leu Lys Asp Ala Thr Ile Gly Glu Ser Cys Tyr Lys Glu
                85                  90                  95
Glu His Asn Pro Ile Ile Lys Lys Pro Ser His Asn Glu Pro Asp Gln
            100                 105                 110
Arg Leu Tyr Ile Asn His Ser Ala Tyr Phe Arg Gly Val Ser Gln Glu
        115                 120                 125
Ile Tyr Asp Tyr Arg Ile Gly Gly Tyr Gly Val Leu Asp Lys Tyr Leu
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   130                 135                 140
Lys Ser His Lys Asn Glu Pro Cys Asp Phe Asp His Val Thr Asn Ile
145                 150                 155                 160
Ile Lys Val Ile Ala Arg Thr Ile Glu Ile Gln Lys Thr Leu Gly Phe
                165                 170                 175
Leu Thr Ser Asp Leu Pro His Leu Lys Gly Asn Asp Ser Lys Ala Leu
            180                 185                 190
Met Gln Glu Ile Leu Gln Asn Pro Pro Pro Pro Pro Pro Ile
        195                 200                 205
<210> 253
<211> 1269
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(1269)
<400> 253
ttt gac aga gaa aga atc cct gaa agg gtg gtg cat gct aaa gga agc   48
Phe Asp Arg Glu Arg Ile Pro Glu Arg Val Val His Ala Lys Gly Ser
  1               5                  10                  15
gga gct tat ggc act ttc act gtg act aaa gac atc act aaa tac act   96
Gly Ala Tyr Gly Thr Phe Thr Val Thr Lys Asp Ile Thr Lys Tyr Thr
             20                  25                  30
aaa gcg aaa att ttc tct aaa gtg ggc aaa aaa acc gaa tgc ttc ttc  144
Lys Ala Lys Ile Phe Ser Lys Val Gly Lys Lys Thr Glu Cys Phe Phe
         35                  40                  45
aga ttt tct act gtg gct ggt gaa aga ggc agt gcg gat gcg gtg aga  192
Arg Phe Ser Thr Val Ala Gly Glu Arg Gly Ser Ala Asp Ala Val Arg
     50                  55                  60
gac cct aga ggt ttt gcg atg aag tat tac act gaa gaa ggt aac tgg  240
Asp Pro Arg Gly Phe Ala Met Lys Tyr Tyr Thr Glu Glu Gly Asn Trp
 65                  70                  75                  80
gat tta gtg ggg aac aac acg cct gtt ttc ttt atc cgt gat gcg atc  288
Asp Leu Val Gly Asn Asn Thr Pro Val Phe Phe Ile Arg Asp Ala Ile
                 85                  90                  95
aaa ttc cct gat ttc atc cac act caa aaa cga gat cct caa acc aat  336
Lys Phe Pro Asp Phe Ile His Thr Gln Lys Arg Asp Pro Gln Thr Asn
            100                 105                 110
ttg cct aac cat gac atg gta tgg gat ttt tgg agt aat gtt cct gaa  384
Leu Pro Asn His Asp Met Val Trp Asp Phe Trp Ser Asn Val Pro Glu
        115                 120                 125
agc tta tac caa gta aca tgg gtt atg agc gat agg ggt att cct aaa  432
Ser Leu Tyr Gln Val Thr Trp Val Met Ser Asp Arg Gly Ile Pro Lys
    130                 135                 140
tct ttc cgc cac atg gat ggt ttt ggc agc cac act ttc agt ctt atc  480
Ser Phe Arg His Met Asp Gly Phe Gly Ser His Thr Phe Ser Leu Ile
145                 150                 155                 160
aac gcg aaa ggc gaa cgc ttt tgg gtg aaa ttc cac ttt cac acc atg  528
Asn Ala Lys Gly Glu Arg Phe Trp Val Lys Phe His Phe His Thr Met
                165                 170                 175
caa ggc gtt aag cat ttg act aac gaa gaa gcc gca gaa gtt agg aag  576
Gln Gly Val Lys His Leu Thr Asn Glu Glu Ala Ala Glu Val Arg Lys
            180                 185                 190
tat gat ccg gat tcc aat caa agg gat tta ttc aat gcg atc gct aga  624
Tyr Asp Pro Asp Ser Asn Gln Arg Asp Leu Phe Asn Ala Ile Ala Arg
        195                 200                 205
ggg gat ttc cca aaa tgg aaa tta agc att caa gtg atg cca gaa gaa  672
Gly Asp Phe Pro Lys Trp Lys Leu Ser Ile Gln Val Met Pro Glu Glu
    210                 215                 220
gat gct aag aag tat cga ttc cat ccg ttt gat gta act aaa att tgg  720
Asp Ala Lys Lys Tyr Arg Phe His Pro Phe Asp Val Thr Lys Ile Trp
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225                 230                 235                 240
tat ctc caa gat tat cca ttg atg gaa gtg ggc att gtg gag ttg aat   768
Tyr Leu Gln Asp Tyr Pro Leu Met Glu Val Gly Ile Val Glu Leu Asn
                245                 250                 255
aaa aat cct gaa aac tat ttc gca gaa gtg gaa caa gcg gca ttc agt   816
Lys Asn Pro Glu Asn Tyr Phe Ala Glu Val Glu Gln Ala Ala Phe Ser
            260                 265                 270
ccg gct aat gtc gtt cct gga att ggc tat agc cct gat agg atg tta   864
Pro Ala Asn Val Val Pro Gly Ile Gly Tyr Ser Pro Asp Arg Met Leu
        275                 280                 285
caa ggg cgc ttg ttc tct tat gga gac aca cac cgc tac cgc tta ggc   912
Gln Gly Arg Leu Phe Ser Tyr Gly Asp Thr His Arg Tyr Arg Leu Gly
    290                 295                 300
gtt aat tat cct caa ata ccg gtt aat aaa cca aga tgc cca ttc cac   960
Val Asn Tyr Pro Gln Ile Pro Val Asn Lys Pro Arg Cys Pro Phe His
305                 310                 315                 320
tct tct agc aga gat ggt tac atg caa aac gga tac tac ggc tct tta  1008
Ser Ser Ser Arg Asp Gly Tyr Met Gln Asn Gly Tyr Tyr Gly Ser Leu
                325                 330                 335
caa aac tat acg cct agc tca ttg cct ggc tat aaa gaa gat aag agc  1056
Gln Asn Tyr Thr Pro Ser Ser Leu Pro Gly Tyr Lys Glu Asp Lys Ser
            340                 345                 350
gcg aga gat cct aag ttc aac tta gct cat att gag aaa gag ttt gaa  1104
Ala Arg Asp Pro Lys Phe Asn Leu Ala His Ile Glu Lys Glu Phe Glu
        355                 360                 365
gtg tgg aat tgg gat tac aga gct gat gat agc gat tac tac acc caa  1152
Val Trp Asn Trp Asp Tyr Arg Ala Asp Asp Ser Asp Tyr Tyr Thr Gln
    370                 375                 380
cca ggt gat tac tac cgc tca ttg cca gct gat gaa aaa gaa agg ttg  1200
Pro Gly Asp Tyr Tyr Arg Ser Leu Pro Ala Asp Glu Lys Glu Arg Leu
385                 390                 395                 400
cat gac act att gga gag tct tta gct cat gtt acc cat aag gaa att  1248
His Asp Thr Ile Gly Glu Ser Leu Ala His Val Thr His Lys Glu Ile
                405                 410                 415
gtg gat aaa caa ttg gag cat                                     1269
Val Asp Lys Gln Leu Glu His
            420
<210> 254
<211> 423
<212> PRT
<213> Helicobacter pylori
<400> 254
Phe Asp Arg Glu Arg Ile Pro Glu Arg Val Val His Ala Lys Gly Ser
  1               5                  10                  15
Gly Ala Tyr Gly Thr Phe Thr Val Thr Lys Asp Ile Thr Lys Tyr Thr
            20                  25                  30
Lys Ala Lys Ile Phe Ser Lys Val Gly Lys Lys Thr Glu Cys Phe Phe
        35                  40                  45
Arg Phe Ser Thr Val Ala Gly Glu Arg Gly Ser Ala Asp Ala Val Arg
    50                  55                  60
Asp Pro Arg Gly Phe Ala Met Lys Tyr Tyr Thr Glu Glu Gly Asn Trp
65                  70                  75                  80
Asp Leu Val Gly Asn Asn Thr Pro Val Phe Phe Ile Arg Asp Ala Ile
                85                  90                  95
Lys Phe Pro Asp Phe Ile His Thr Gln Lys Arg Asp Pro Gln Thr Asn
            100                 105                 110
Leu Pro Asn His Asp Met Val Trp Asp Phe Trp Ser Asn Val Pro Glu
        115                 120                 125
Ser Leu Tyr Gln Val Thr Trp Val Met Ser Asp Arg Gly Ile Pro Lys
    130                 135                 140
Ser Phe Arg His Met Asp Gly Phe Gly Ser His Thr Phe Ser Leu Ile
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145                 150                 155                 160
Asn Ala Lys Gly Glu Arg Phe Trp Val Lys Phe His Phe His Thr Met
                165                 170                 175
Gln Gly Val Lys His Leu Thr Asn Glu Glu Ala Ala Glu Val Arg Lys
            180                 185                 190
Tyr Asp Pro Asp Ser Asn Gln Arg Asp Leu Phe Asn Ala Ile Ala Arg
        195                 200                 205
Gly Asp Phe Pro Lys Trp Lys Leu Ser Ile Gln Val Met Pro Glu Glu
    210                 215                 220
Asp Ala Lys Lys Tyr Arg Phe His Pro Phe Asp Val Thr Lys Ile Trp
225                 230                 235                 240
Tyr Leu Gln Asp Tyr Pro Leu Met Glu Val Gly Ile Val Glu Leu Asn
                245                 250                 255
Lys Asn Pro Glu Asn Tyr Phe Ala Glu Val Glu Gln Ala Ala Phe Ser
            260                 265                 270
Pro Ala Asn Val Val Pro Gly Ile Gly Tyr Ser Pro Asp Arg Met Leu
        275                 280                 285
Gln Gly Arg Leu Phe Ser Tyr Gly Asp Thr His Arg Tyr Arg Leu Gly
    290                 295                 300
Val Asn Tyr Pro Gln Ile Pro Val Asn Lys Pro Arg Cys Pro Phe His
305                 310                 315                 320
Ser Ser Ser Arg Asp Gly Tyr Met Gln Asn Gly Tyr Tyr Gly Ser Leu
                325                 330                 335
Gln Asn Tyr Thr Pro Ser Ser Leu Pro Gly Tyr Lys Glu Asp Lys Ser
            340                 345                 350
Ala Arg Asp Pro Lys Phe Asn Leu Ala His Ile Glu Lys Glu Phe Glu
        355                 360                 365
Val Trp Asn Trp Asp Tyr Arg Ala Asp Asp Ser Asp Tyr Tyr Thr Gln
    370                 375                 380
Pro Gly Asp Tyr Tyr Arg Ser Leu Pro Ala Asp Glu Lys Glu Arg Leu
385                 390                 395                 400
His Asp Thr Ile Gly Glu Ser Leu Ala His Val Thr His Lys Glu Ile
                405                 410                 415
Val Asp Lys Gln Leu Glu His
            420
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<210> 255
<211> 1005
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(1005)
<400> 255

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agc att att tat ccc ctt tat atg ggt ggg gca aga ttc acg atg gtg   48
Ser Ile Ile Tyr Pro Leu Tyr Met Gly Gly Ala Arg Phe Thr Met Val
  1               5                  10                  15
cgc att gcg gat ttg atg caa aaa gat gct aat gaa gtg tat cgt ttg   96
Arg Ile Ala Asp Leu Met Gln Lys Asp Ala Asn Glu Val Tyr Arg Leu
             20                  25                  30
aaa aag ctt tcc act ttt caa gag ctt gtg agc gtg tat tac ggc atg   144
Lys Lys Leu Ser Thr Phe Gln Glu Leu Val Ser Val Tyr Tyr Gly Met
         35                  40                  45
gtg tta aac gca gaa gtg gct gaa act tta gaa gag gtg gaa aaa ggc   192
Val Leu Asn Ala Glu Val Ala Glu Thr Leu Glu Glu Val Glu Lys Gly
     50                  55                  60
cat tat aag cat ttc caa aac gct ttg aaa atg caa aaa gtg ggg caa   240
His Tyr Lys His Phe Gln Asn Ala Leu Lys Met Gln Lys Val Gly Gln
 65                  70                  75                  80
atc gct agg gta gaa acc tta ggc gct caa gtg gct tat gat aag gcc   288
Ile Ala Arg Val Glu Thr Leu Gly Ala Gln Val Ala Tyr Asp Lys Ala
                 85                  90                  95
```

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cat atc gct agc gtt aag gct aaa gac gtg tta gaa gtt tcg cag ctc   336
His Ile Ala Ser Val Lys Ala Lys Asp Val Leu Glu Val Ser Gln Leu
            100                 105                 110
tcg ttc aat tcc att tta tct agc aag gac gat tta gtg cct tca agc   384
Ser Phe Asn Ser Ile Leu Ser Ser Lys Asp Asp Leu Val Pro Ser Ser
        115                 120                 125
aaa tta gag atc cgc acg gag aaa aat ctg ccc gat ctg agc ttt ttt   432
Lys Leu Glu Ile Arg Thr Glu Lys Asn Leu Pro Asp Leu Ser Phe Phe
    130                 135                 140
gtt tct tcc acg ctc aat tcc tac ccg gtt tta aag act tta gaa aat   480
Val Ser Ser Thr Leu Asn Ser Tyr Pro Val Leu Lys Thr Leu Glu Asn
145                 150                 155                 160
cag att caa atc tct aaa gaa aac acg aaa tta cag atc gct aaa ttc   528
Gln Ile Gln Ile Ser Lys Glu Asn Thr Lys Leu Gln Ile Ala Lys Phe
                165                 170                 175
ttg ccc caa gtg agt ttt ttt ggc tct tat att atg aag caa aac aat   576
Leu Pro Gln Val Ser Phe Phe Gly Ser Tyr Ile Met Lys Gln Asn Asn
            180                 185                 190
tcg gtg ttt gaa gac atg atc cct agt tgg ttt gtg ggc gtg gcc ggg   624
Ser Val Phe Glu Asp Met Ile Pro Ser Trp Phe Val Gly Val Ala Gly
        195                 200                 205
cgc atg cct att ctt tct ccc aca ggg cgc att caa aaa tac caa gcg   672
Arg Met Pro Ile Leu Ser Pro Thr Gly Arg Ile Gln Lys Tyr Gln Ala
    210                 215                 220
agc aaa tta gcg gag ttg caa gtg agt agc gaa caa atc cag gct aaa   720
Ser Lys Leu Ala Glu Leu Gln Val Ser Ser Glu Gln Ile Gln Ala Lys
225                 230                 235                 240
aaa aac atg gaa tta tta gtg aat aag act tat aaa gag acg ctt tct   768
Lys Asn Met Glu Leu Leu Val Asn Lys Thr Tyr Lys Glu Thr Leu Ser
                245                 250                 255
tat ttg aaa gaa tac aaa agc ttg ctt tct agc gtg gaa tta gcc aag   816
Tyr Leu Lys Glu Tyr Lys Ser Leu Leu Ser Ser Val Glu Leu Ala Lys
            260                 265                 270
gaa aac tta aaa ctc caa gag cag gct ttt tta caa ggc tta agc acg   864
Glu Asn Leu Lys Leu Gln Glu Gln Ala Phe Leu Gln Gly Leu Ser Thr
        275                 280                 285
aac gct caa gtc att gat gcg agg aac acg ctt tct tct atc gtc gtg   912
Asn Ala Gln Val Ile Asp Ala Arg Asn Thr Leu Ser Ser Ile Val Val
    290                 295                 300
gag caa aaa agc gtg gct tat aaa tac atc gtt tca tta gcg aat tta   960
Glu Gln Lys Ser Val Ala Tyr Lys Tyr Ile Val Ser Leu Ala Asn Leu
305                 310                 315                 320
atg gcg tta agc gat cat att gat tta ttt tat gaa ttt gtt tat      1005
Met Ala Leu Ser Asp His Ile Asp Leu Phe Tyr Glu Phe Val Tyr
                325                 330                 335
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<210> 256
<211> 335
<212> PRT
<213> Helicobacter pylori
<400> 256

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Ser Ile Ile Tyr Pro Leu Tyr Met Gly Gly Ala Arg Phe Thr Met Val
  1               5                  10                  15
Arg Ile Ala Asp Leu Met Gln Lys Asp Ala Asn Glu Val Tyr Arg Leu
             20                  25                  30
Lys Lys Leu Ser Thr Phe Gln Glu Leu Val Ser Val Tyr Tyr Gly Met
         35                  40                  45
Val Leu Asn Ala Glu Val Ala Glu Thr Leu Glu Glu Val Glu Lys Gly
     50                  55                  60
His Tyr Lys His Phe Gln Asn Ala Leu Lys Met Gln Lys Val Gly Gln
 65                  70                  75                  80
Ile Ala Arg Val Glu Thr Leu Gly Ala Gln Val Ala Tyr Asp Lys Ala
```

```
                85                  90                  95
His Ile Ala Ser Val Lys Ala Lys Asp Val Leu Glu Val Ser Gln Leu
            100                 105                 110
Ser Phe Asn Ser Ile Leu Ser Ser Lys Asp Asp Leu Val Pro Ser Ser
        115                 120                 125
Lys Leu Glu Ile Arg Thr Glu Lys Asn Leu Pro Asp Leu Ser Phe Phe
    130                 135                 140
Val Ser Ser Thr Leu Asn Ser Tyr Pro Val Leu Lys Thr Leu Glu Asn
145                 150                 155                 160
Gln Ile Gln Ile Ser Lys Glu Asn Thr Lys Leu Gln Ile Ala Lys Phe
                165                 170                 175
Leu Pro Gln Val Ser Phe Phe Gly Ser Tyr Ile Met Lys Gln Asn Asn
            180                 185                 190
Ser Val Phe Glu Asp Met Ile Pro Ser Trp Phe Val Gly Val Ala Gly
        195                 200                 205
Arg Met Pro Ile Leu Ser Pro Thr Gly Arg Ile Gln Lys Tyr Gln Ala
    210                 215                 220
Ser Lys Leu Ala Glu Leu Gln Val Ser Ser Glu Gln Ile Gln Ala Lys
225                 230                 235                 240
Lys Asn Met Glu Leu Leu Val Asn Lys Thr Tyr Lys Glu Thr Leu Ser
                245                 250                 255
Tyr Leu Lys Glu Tyr Lys Ser Leu Leu Ser Ser Val Glu Leu Ala Lys
            260                 265                 270
Glu Asn Leu Lys Leu Gln Glu Gln Ala Phe Leu Gln Gly Leu Ser Thr
        275                 280                 285
Asn Ala Gln Val Ile Asp Ala Arg Asn Thr Leu Ser Ser Ile Val Val
    290                 295                 300
Glu Gln Lys Ser Val Ala Tyr Lys Tyr Ile Val Ser Leu Ala Asn Leu
305                 310                 315                 320
Met Ala Leu Ser Asp His Ile Asp Leu Phe Tyr Glu Phe Val Tyr
                325                 330                 335

<210> 257
<211> 296
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(294)
<400> 257
gaa atc att aga gat att gct gat caa acc aat ctt tta gcc tta aac   48
Glu Ile Ile Arg Asp Ile Ala Asp Gln Thr Asn Leu Leu Ala Leu Asn
  1               5                  10                  15
gcc gct att gaa gcc gca agg gcc ggc gag cat ggc aga ggc ttt gcg   96
Ala Ala Ile Glu Ala Ala Arg Ala Gly Glu His Gly Arg Gly Phe Ala
             20                  25                  30
gtg gtg gct gat gag gta aga aag ctc gct gaa agg acg caa aaa tcg   144
Val Val Ala Asp Glu Val Arg Lys Leu Ala Glu Arg Thr Gln Lys Ser
         35                  40                  45
ctc agc gag att gaa gcc aat atc aat att tta gtg caa agc att tca   192
Leu Ser Glu Ile Glu Ala Asn Ile Asn Ile Leu Val Gln Ser Ile Ser
     50                  55                  60
gac acg agc gaa agc att aaa aac cag gtt aaa gaa gtg gaa gaa atc   240
Asp Thr Ser Glu Ser Ile Lys Asn Gln Val Lys Glu Val Glu Glu Ile
 65                  70                  75                  80
aac gct tct att gaa gcc tta aga tcg gtt act gag ggc aat cta aaa   288
Asn Ala Ser Ile Glu Ala Leu Arg Ser Val Thr Glu Gly Asn Leu Lys
                 85                  90                  95
atc gct ag                                                       296
Ile Ala
<210> 258
<211> 98
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<212> PRT
<213> Helicobacter pylori
<400> 258
Glu Ile Ile Arg Asp Ile Ala Asp Gln Thr Asn Leu Leu Ala Leu Asn
1 5 10 15
Ala Ala Ile Glu Ala Ala Arg Ala Gly Glu His Gly Arg Gly Phe Ala
20 25 30
Val Val Ala Asp Glu Val Arg Lys Leu Ala Glu Arg Thr Gln Lys Ser
35 40 45
Leu Ser Glu Ile Glu Ala Asn Ile Asn Ile Leu Val Gln Ser Ile Ser
50 55 60
Asp Thr Ser Glu Ser Ile Lys Asn Gln Val Lys Glu Val Glu Glu Ile
65 70 75 80
Asn Ala Ser Ile Glu Ala Leu Arg Ser Val Thr Glu Gly Asn Leu Lys
85 90 95
Ile Ala
<210> 259
<211> 430
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(429)
<400> 259
att caa gct tta ctc gtg ggc gtt caa gaa gaa tat tac gct atc ccg 48
Ile Gln Ala Leu Leu Val Gly Val Gln Glu Glu Tyr Tyr Ala Ile Pro
1 5 10 15
ctt tct tca gtg tta gaa acc gtg cgc atc agc cag gat gaa att tac 96
Leu Ser Ser Val Leu Glu Thr Val Arg Ile Ser Gln Asp Glu Ile Tyr
20 25 30
acc gtt gat ggc aag agc gtg ttg cgt ttg aga gat gag gtg ctt tct 144
Thr Val Asp Gly Lys Ser Val Leu Arg Leu Arg Asp Glu Val Leu Ser
35 40 45
ttg gtg cgc ctt tct gat att ttt aaa gta gat gct att ttg gaa tcc 192
Leu Val Arg Leu Ser Asp Ile Phe Lys Val Asp Ala Ile Leu Glu Ser
50 55 60
aac tca gat gtg tat gtg gtt atc att ggc ttg gct gat caa aaa att 240
Asn Ser Asp Val Tyr Val Val Ile Ile Gly Leu Ala Asp Gln Lys Ile
65 70 75 80
ggc gtg atc gtg gat tat tta atc ggt caa gaa gaa gtg gtc att aaa 288
Gly Val Ile Val Asp Tyr Leu Ile Gly Gln Glu Glu Val Val Ile Lys
85 90 95
tct tta ggt tac tat ctt aaa aac act aga ggc att gct ggt gct acg 336
Ser Leu Gly Tyr Tyr Leu Lys Asn Thr Arg Gly Ile Ala Gly Ala Thr
100 105 110
gtg aga ggc gat ggg aaa atc acc ctt att gta gat gtg ggg gcg atg 384
Val Arg Gly Asp Gly Lys Ile Thr Leu Ile Val Asp Val Gly Ala Met
115 120 125
atg gat atg gca aaa agc atc aag gtc aat atc act acc tta atg a 430
Met Asp Met Ala Lys Ser Ile Lys Val Asn Ile Thr Thr Leu Met
130 135 140
<210> 260
<211> 143
<212> PRT
<213> Helicobacter pylori
<400> 260
Ile Gln Ala Leu Leu Val Gly Val Gln Glu Glu Tyr Tyr Ala Ile Pro
1 5 10 15
Leu Ser Ser Val Leu Glu Thr Val Arg Ile Ser Gln Asp Glu Ile Tyr
20 25 30
Thr Val Asp Gly Lys Ser Val Leu Arg Leu Arg Asp Glu Val Leu Ser

```
        35                  40                  45
Leu Val Arg Leu Ser Asp Ile Phe Lys Val Asp Ala Ile Leu Glu Ser
    50                  55                  60
Asn Ser Asp Val Tyr Val Val Ile Ile Gly Leu Ala Asp Gln Lys Ile
65                  70                  75                  80
Gly Val Ile Val Asp Tyr Leu Ile Gly Gln Glu Glu Val Val Ile Lys
                85                  90                  95
Ser Leu Gly Tyr Tyr Leu Lys Asn Thr Arg Gly Ile Ala Gly Ala Thr
            100                 105                 110
Val Arg Gly Asp Gly Lys Ile Thr Leu Ile Val Asp Val Gly Ala Met
        115                 120                 125
Met Asp Met Ala Lys Ser Ile Lys Val Asn Ile Thr Thr Leu Met
    130                 135                 140
<210> 261
<211> 497
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(495)
<400> 261
aaa att gga gtt tgt ggt cct gta gga agc ggt aaa acc gcc ttg att   48
Lys Ile Gly Val Cys Gly Pro Val Gly Ser Gly Lys Thr Ala Leu Ile
  1               5                  10                  15
gaa gct tta acg cgc cac atg tca aaa gat tat gac atg gcg gtc atc   96
Glu Ala Leu Thr Arg His Met Ser Lys Asp Tyr Asp Met Ala Val Ile
            20                  25                  30
act aat gat att tac acg aaa gaa gac gca gag ttt atg tgt aaa aat   144
Thr Asn Asp Ile Tyr Thr Lys Glu Asp Ala Glu Phe Met Cys Lys Asn
        35                  40                  45
tcg gtg atg cca cga gag agg atc att ggc gta gaa aca gga ggc tgt   192
Ser Val Met Pro Arg Glu Arg Ile Ile Gly Val Glu Thr Gly Gly Cys
    50                  55                  60
ccg cac acg gct att aga gaa gac gct tct atg aat tta gaa gcc gta   240
Pro His Thr Ala Ile Arg Glu Asp Ala Ser Met Asn Leu Glu Ala Val
65                  70                  75                  80
gaa gaa atg cat ggc cgt ttc cct aat ttg gaa ttg ctt ttg att gaa   288
Glu Glu Met His Gly Arg Phe Pro Asn Leu Glu Leu Leu Leu Ile Glu
                85                  90                  95
agc gga ggc gat aac ctt tca gcg aca ttc aac cca gag cta gcg gac   336
Ser Gly Gly Asp Asn Leu Ser Ala Thr Phe Asn Pro Glu Leu Ala Asp
            100                 105                 110
ttt acg atc ttt gtg att gat gtg gct gag ggc gat aaa atc ccc cga   384
Phe Thr Ile Phe Val Ile Asp Val Ala Glu Gly Asp Lys Ile Pro Arg
        115                 120                 125
aaa ggc ggg cca gga atc acg cgc tca gac ttg ctt gtc atc aat aag   432
Lys Gly Gly Pro Gly Ile Thr Arg Ser Asp Leu Leu Val Ile Asn Lys
    130                 135                 140
att gat tta gcc ccc tat gtg gga gcg gac ttg aaa gtc atg gaa agg   480
Ile Asp Leu Ala Pro Tyr Val Gly Ala Asp Leu Lys Val Met Glu Arg
145                 150                 155                 160
gat tct aaa aaa atg cg                                           497
Asp Ser Lys Lys Met
                165
<210> 262
<211> 165
<212> PRT
<213> Helicobacter pylori
<400> 262
Lys Ile Gly Val Cys Gly Pro Val Gly Ser Gly Lys Thr Ala Leu Ile
  1               5                  10                  15
```

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Glu Ala Leu Thr Arg His Met Ser Lys Asp Tyr Asp Met Ala Val Ile
                20                  25                  30
Thr Asn Asp Ile Tyr Thr Lys Glu Asp Ala Glu Phe Met Cys Lys Asn
            35                  40                  45
Ser Val Met Pro Arg Glu Arg Ile Ile Gly Val Glu Thr Gly Gly Cys
        50                  55                  60
Pro His Thr Ala Ile Arg Glu Asp Ala Ser Met Asn Leu Glu Ala Val
65                  70                  75                  80
Glu Glu Met His Gly Arg Phe Pro Asn Leu Glu Leu Leu Leu Ile Glu
                85                  90                  95
Ser Gly Gly Asp Asn Leu Ser Ala Thr Phe Asn Pro Glu Leu Ala Asp
            100                 105                 110
Phe Thr Ile Phe Val Ile Asp Val Ala Glu Gly Asp Lys Ile Pro Arg
        115                 120                 125
Lys Gly Gly Pro Gly Ile Thr Arg Ser Asp Leu Leu Val Ile Asn Lys
    130                 135                 140
Ile Asp Leu Ala Pro Tyr Val Gly Ala Asp Leu Lys Val Met Glu Arg
145                 150                 155                 160
Asp Ser Lys Lys Met
                165
<210> 263
<211> 402
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(402)
<400> 263
ttt aaa acc agg caa ggc aaa gac ata gcc ata cgc ctt aaa gac gct   48
Phe Lys Thr Arg Gln Gly Lys Asp Ile Ala Ile Arg Leu Lys Asp Ala
  1               5                  10                  15
ccc aag ttg ggg ctc tct caa ggg gat att tta ttt aaa gaa gag aag   96
Pro Lys Leu Gly Leu Ser Gln Gly Asp Ile Leu Phe Lys Glu Glu Lys
             20                  25                  30
gaa att atc gcc gtt aat atc ttg gat tct gaa gtc att cac atc caa   144
Glu Ile Ile Ala Val Asn Ile Leu Asp Ser Glu Val Ile His Ile Gln
         35                  40                  45
gcc aag agc gtg gca gaa gta gcg aaa ata tgc tat gaa ata gga aac   192
Ala Lys Ser Val Ala Glu Val Ala Lys Ile Cys Tyr Glu Ile Gly Asn
     50                  55                  60
cgc cat gcg gct tta tac tat ggc gag tct caa ttt gaa ttt aaa aca   240
Arg His Ala Ala Leu Tyr Tyr Gly Glu Ser Gln Phe Glu Phe Lys Thr
 65                  70                  75                  80
cca ttt gaa aag ccc acg cta gcg tta tta gaa aag cta ggg gtt caa   288
Pro Phe Glu Lys Pro Thr Leu Ala Leu Leu Glu Lys Leu Gly Val Gln
                85                  90                  95
aat cgt gtt tta agt tca aaa ttg gat tcc aaa gaa cgc tta acc gtg   336
Asn Arg Val Leu Ser Ser Lys Leu Asp Ser Lys Glu Arg Leu Thr Val
            100                 105                 110
agc atg ccc cat agt gag cct aat ttt aag gtc tca cta gcg agc gat   384
Ser Met Pro His Ser Glu Pro Asn Phe Lys Val Ser Leu Ala Ser Asp
        115                 120                 125
ttt aaa gtg gtc gta aaa                                          402
Phe Lys Val Val Val Lys
    130
<210> 264
<211> 134
<212> PRT
<213> Helicobacter pylori
<400> 264
Phe Lys Thr Arg Gln Gly Lys Asp Ile Ala Ile Arg Leu Lys Asp Ala
```

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 1               5                  10                  15
Pro Lys Leu Gly Leu Ser Gln Gly Asp Ile Leu Phe Lys Glu Glu Lys
            20                  25                  30
Glu Ile Ile Ala Val Asn Ile Leu Asp Ser Glu Val Ile His Ile Gln
        35                  40                  45
Ala Lys Ser Val Ala Glu Val Ala Lys Ile Cys Tyr Glu Ile Gly Asn
    50                  55                  60
Arg His Ala Ala Leu Tyr Tyr Gly Glu Ser Gln Phe Glu Phe Lys Thr
65                  70                  75                  80
Pro Phe Glu Lys Pro Thr Leu Ala Leu Leu Glu Lys Leu Gly Val Gln
                85                  90                  95
Asn Arg Val Leu Ser Ser Lys Leu Asp Ser Lys Glu Arg Leu Thr Val
            100                 105                 110
Ser Met Pro His Ser Glu Pro Asn Phe Lys Val Ser Leu Ala Ser Asp
        115                 120                 125
Phe Lys Val Val Val Lys
    130
<210> 265
<211> 606
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(606)
<400> 265
att aaa aga gcg gca aag gaa ttg aaa gag ggc atg tat gtg aat tta   48
Ile Lys Arg Ala Ala Lys Glu Leu Lys Glu Gly Met Tyr Val Asn Leu
 1               5                  10                  15
ggg ata ggc ttg ccc acg ctt gtg gct aat gaa gtg agc ggg atg aat   96
Gly Ile Gly Leu Pro Thr Leu Val Ala Asn Glu Val Ser Gly Met Asn
            20                  25                  30
atc gtt ttc caa agc gag aac ggg ctg tta ggg att ggc gct tac cct  144
Ile Val Phe Gln Ser Glu Asn Gly Leu Leu Gly Ile Gly Ala Tyr Pro
        35                  40                  45
tta gag ggg agc gtt gat gcg gat ctt atc aac gca gga aag gaa acc  192
Leu Glu Gly Ser Val Asp Ala Asp Leu Ile Asn Ala Gly Lys Glu Thr
    50                  55                  60
ata acc gtg gtg ccg ggc gct tcg ttt ttc aat agc gcg gat tcg ttt  240
Ile Thr Val Val Pro Gly Ala Ser Phe Phe Asn Ser Ala Asp Ser Phe
65                  70                  75                  80
gcg atg att cgt ggg ggg cat att gat tta gcg att tta ggg ggg atg  288
Ala Met Ile Arg Gly Gly His Ile Asp Leu Ala Ile Leu Gly Gly Met
                85                  90                  95
gaa gtc tca caa aat ggg gat ttg gct aat tgg atg atc cct aaa aag  336
Glu Val Ser Gln Asn Gly Asp Leu Ala Asn Trp Met Ile Pro Lys Lys
            100                 105                 110
ctc ata aag ggc atg gga ggg gct atg gat ttg gtg cat ggc gct aaa  384
Leu Ile Lys Gly Met Gly Gly Ala Met Asp Leu Val His Gly Ala Lys
        115                 120                 125
aaa gtg att gtg atc atg gag cat tgc aac aaa tac ggg gag tct aaa  432
Lys Val Ile Val Ile Met Glu His Cys Asn Lys Tyr Gly Glu Ser Lys
    130                 135                 140
gtg aaa aag gaa tgc tca ttg ccc tta aca gga aaa ggc gtg gtg cat  480
Val Lys Lys Glu Cys Ser Leu Pro Leu Thr Gly Lys Gly Val Val His
145                 150                 155                 160
caa ttg ata acg gat tta gcg gtg ttt gag ttt tcc aat aac gcc atg  528
Gln Leu Ile Thr Asp Leu Ala Val Phe Glu Phe Ser Asn Asn Ala Met
                165                 170                 175
aaa tta gtg gaa ttg caa gag ggg gtc agc ctt gat caa gtg aaa gaa  576
Lys Leu Val Glu Leu Gln Glu Gly Val Ser Leu Asp Gln Val Lys Glu
            180                 185                 190
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aag aca gaa gct gaa ttt gag gtg cgc tta 606
Lys Thr Glu Ala Glu Phe Glu Val Arg Leu
195 200

<210> 266
<211> 202
<212> PRT
<213> Helicobacter pylori
<400> 266
Ile Lys Arg Ala Ala Lys Glu Leu Lys Glu Gly Met Tyr Val Asn Leu
1 5 10 15
Gly Ile Gly Leu Pro Thr Leu Val Ala Asn Glu Val Ser Gly Met Asn
20 25 30
Ile Val Phe Gln Ser Glu Asn Gly Leu Leu Gly Ile Gly Ala Tyr Pro
35 40 45
Leu Glu Gly Ser Val Asp Ala Asp Leu Ile Asn Ala Gly Lys Glu Thr
50 55 60
Ile Thr Val Val Pro Gly Ala Ser Phe Phe Asn Ser Ala Asp Ser Phe
65 70 75 80
Ala Met Ile Arg Gly Gly His Ile Asp Leu Ala Ile Leu Gly Gly Met
85 90 95
Glu Val Ser Gln Asn Gly Asp Leu Ala Asn Trp Met Ile Pro Lys Lys
100 105 110
Leu Ile Lys Gly Met Gly Gly Ala Met Asp Leu Val His Gly Ala Lys
115 120 125
Lys Val Ile Val Ile Met Glu His Cys Asn Lys Tyr Gly Glu Ser Lys
130 135 140
Val Lys Lys Glu Cys Ser Leu Pro Leu Thr Gly Lys Gly Val Val His
145 150 155 160
Gln Leu Ile Thr Asp Leu Ala Val Phe Glu Phe Ser Asn Asn Ala Met
165 170 175
Lys Leu Val Glu Leu Gln Glu Gly Val Ser Leu Asp Gln Val Lys Glu
180 185 190
Lys Thr Glu Ala Glu Phe Glu Val Arg Leu
195 200

<210> 267
<211> 336
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(336)
<400> 267
ggg att gaa caa gac gct gat att gtt tta ttt tta tat aga ggc tat 48
Gly Ile Glu Gln Asp Ala Asp Ile Val Leu Phe Leu Tyr Arg Gly Tyr
1 5 10 15
atc tat caa atg agg gct gaa gac aac aaa ata gac aaa ctc aaa aaa 96
Ile Tyr Gln Met Arg Ala Glu Asp Asn Lys Ile Asp Lys Leu Lys Lys
20 25 30
gaa ggt aaa att gaa gag gcg caa gag ttg tac tta aaa gtt aat gaa 144
Glu Gly Lys Ile Glu Glu Ala Gln Glu Leu Tyr Leu Lys Val Asn Glu
35 40 45
gaa agg cgt atc cac aag caa aat ggc agc att gaa gag gct gaa atc 192
Glu Arg Arg Ile His Lys Gln Asn Gly Ser Ile Glu Glu Ala Glu Ile
50 55 60
att gtg gct aaa aac agg aat ggg gct aca gga acg gtt tat acg cgc 240
Ile Val Ala Lys Asn Arg Asn Gly Ala Thr Gly Thr Val Tyr Thr Arg
65 70 75 80
ttt aac gct cct ttc acg cgc tat gaa gac atg ccc ata gat tcc cat 288
Phe Asn Ala Pro Phe Thr Arg Tyr Glu Asp Met Pro Ile Asp Ser His
85 90 95
tta gaa gaa ggg caa gaa act aaa gtg gat tat gat ata gtt aca act 336

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Ile Tyr Gln Met Arg Ala Glu Asp Asn Lys Ile Asp Lys Leu Lys Lys
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Glu Gly Lys Ile Glu Glu Ala Gln Glu Leu Tyr Leu Lys Val Asn Glu
         35                  40                  45
Glu Arg Arg Ile His Lys Gln Asn Gly Ser Ile Glu Glu Ala Glu Ile
     50                  55                  60
Ile Val Ala Lys Asn Arg Asn Gly Ala Thr Gly Thr Val Tyr Thr Arg
 65                  70                  75                  80
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            100                 105                 110

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ttg tta gag cat gtc caa aaa gcg ctg aat caa atg agc gaa aga gag   96
Leu Leu Glu His Val Gln Lys Ala Leu Asn Gln Met Ser Glu Arg Glu
             20                  25                  30
caa atc ctt atc cag ctt tat tac ttt gaa gag ttg aat ttg agc gag   144
Gln Ile Leu Ile Gln Leu Tyr Tyr Phe Glu Glu Leu Asn Leu Ser Glu
         35                  40                  45
att aaa gag att tta ggc att act gaa tcg cgc att tct caa atc att   192
Ile Lys Glu Ile Leu Gly Ile Thr Glu Ser Arg Ile Ser Gln Ile Ile
     50                  55                  60
aaa gaa gtg att aaa aag gtg cgt aaa tcc tta gga gtg gat cat ggc   240
Lys Glu Val Ile Lys Lys Val Arg Lys Ser Leu Gly Val Asp His Gly
 65                  70                  75                  80
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<213> Helicobacter pylori
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             20                  25                  30
Gln Ile Leu Ile Gln Leu Tyr Tyr Phe Glu Glu Leu Asn Leu Ser Glu
         35                  40                  45
Ile Lys Glu Ile Leu Gly Ile Thr Glu Ser Arg Ile Ser Gln Ile Ile
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 65                  70                  75                  80
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aat ggc gtg ttt gaa agc agt ggg ggg agg gtg atc ttt gcc att ggt 96
Asn Gly Val Phe Glu Ser Ser Gly Gly Arg Val Ile Phe Ala Ile Gly
20 25 30
agg gga aaa tcc tta tta gaa gcc aga aac cat gct tat gaa atc gct 144
Arg Gly Lys Ser Leu Leu Glu Ala Arg Asn His Ala Tyr Glu Ile Ala
35 40 45
caa aag gtg cat ttt gaa ggc atg ttt tat cgc aag gat att ggt ttt 192
Gln Lys Val His Phe Glu Gly Met Phe Tyr Arg Lys Asp Ile Gly Phe
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aag gtg tta gat ttg aaa gaa tat tct 219
Lys Val Leu Asp Leu Lys Glu Tyr Ser
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Arg Gly Lys Ser Leu Leu Glu Ala Arg Asn His Ala Tyr Glu Ile Ala
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65 70
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Lys Asp Asp Leu Ala Glu Ile Met Leu Leu Ala Val Ser Pro Gly Met
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atg agg ggc gat gcg caa gat gtg caa tta aac atc ggt cca aat tgc 96
Met Arg Gly Asp Ala Gln Asp Val Gln Leu Asn Ile Gly Pro Asn Cys
20 25 30
aag tta agg atc act tcg caa tcc ttt gaa aaa atc cat aac act gaa 144
Lys Leu Arg Ile Thr Ser Gln Ser Phe Glu Lys Ile His Asn Thr Glu
35 40 45
gat ggg ttt gcc agc aga gac atg cat att gtt gtg ggg gaa aac gct 192
Asp Gly Phe Ala Ser Arg Asp Met His Ile Val Val Gly Glu Asn Ala
50 55 60
ttt tta gat ttt gcg cct ttc ccg tta atc ccc ttt gaa aac gcg cat 240
Phe Leu Asp Phe Ala Pro Phe Pro Leu Ile Pro Phe Glu Asn Ala His
65 70 75 80
ttt aag ggc aac acc acg att tct ttg cgc tct agc tct caa ttg ctc 288
Phe Lys Gly Asn Thr Thr Ile Ser Leu Arg Ser Ser Ser Gln Leu Leu

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tat agt gaa atc att gtc gca ggg cga gtg gcg cgc aat gag ttg ttt   336
Tyr Ser Glu Ile Ile Val Ala Gly Arg Val Ala Arg Asn Glu Leu Phe
            100                 105                 110
aaa ttc aac cgc ttg cac acc aaa atc tct att tta caa gat gag aaa   384
Lys Phe Asn Arg Leu His Thr Lys Ile Ser Ile Leu Gln Asp Glu Lys
        115                 120                 125
ccc atc tat tat gac aac acg att tta gat ccc aaa acc acc gac tta   432
Pro Ile Tyr Tyr Asp Asn Thr Ile Leu Asp Pro Lys Thr Thr Asp Leu
    130                 135                 140
aat aac atg tgc atg ttt gat ggc tat acg cat tat ttg aat ttg gtg   480
Asn Asn Met Cys Met Phe Asp Gly Tyr Thr His Tyr Leu Asn Leu Val
145                 150                 155                 160
ctt gtc aat tgc ccc ata gag ctc tct ggt gtg cga gaa tgc att gaa   528
Leu Val Asn Cys Pro Ile Glu Leu Ser Gly Val Arg Glu Cys Ile Glu
                165                 170                 175
gaa agc gaa ggg gtg gat ggg gca gtg agt gaa acc gct agt tct cat   576
Glu Ser Glu Gly Val Asp Gly Ala Val Ser Glu Thr Ala Ser Ser His
            180                 185                 190
tta tgc gtg aaa gct tta gcg aaa ggc tca gaa ccc tta ttg cat tta   624
Leu Cys Val Lys Ala Leu Ala Lys Gly Ser Glu Pro Leu Leu His Leu
        195                 200                 205
aga gaa aaa atc gct cgc ttg gtt acg caa acc acc acg caa aag gtt   672
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            20                  25                  30
Lys Leu Arg Ile Thr Ser Gln Ser Phe Glu Lys Ile His Asn Thr Glu
        35                  40                  45
Asp Gly Phe Ala Ser Arg Asp Met His Ile Val Val Gly Glu Asn Ala
    50                  55                  60
Phe Leu Asp Phe Ala Pro Phe Pro Leu Ile Pro Phe Glu Asn Ala His
65                  70                  75                  80
Phe Lys Gly Asn Thr Thr Ile Ser Leu Arg Ser Ser Ser Gln Leu Leu
                85                  90                  95
Tyr Ser Glu Ile Ile Val Ala Gly Arg Val Ala Arg Asn Glu Leu Phe
            100                 105                 110
Lys Phe Asn Arg Leu His Thr Lys Ile Ser Ile Leu Gln Asp Glu Lys
        115                 120                 125
Pro Ile Tyr Tyr Asp Asn Thr Ile Leu Asp Pro Lys Thr Thr Asp Leu
    130                 135                 140
Asn Asn Met Cys Met Phe Asp Gly Tyr Thr His Tyr Leu Asn Leu Val
145                 150                 155                 160
Leu Val Asn Cys Pro Ile Glu Leu Ser Gly Val Arg Glu Cys Ile Glu
                165                 170                 175
Glu Ser Glu Gly Val Asp Gly Ala Val Ser Glu Thr Ala Ser Ser His
            180                 185                 190
Leu Cys Val Lys Ala Leu Ala Lys Gly Ser Glu Pro Leu Leu His Leu
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Thr His Ile Ile Val Arg Asp Leu Gln Gly Asn Glu Arg Val Leu Ser
            20                  25                  30
aat gaa gag att caa aag ctc atc aaa gaa gaa gaa gct aaa att gat   144
Asn Glu Glu Ile Gln Lys Leu Ile Lys Glu Glu Glu Ala Lys Ile Asp
        35                  40                  45
aac ggc acg agc aag ctt gtc cag cct aat aat gga ggg agt aat gaa   192
Asn Gly Thr Ser Lys Leu Val Gln Pro Asn Asn Gly Gly Ser Asn Glu
    50                  55                  60
ggc tca ggc ttt ggc ttg ggg agc gcg att tta ggg agc gcg gcg ggg   240
Gly Ser Gly Phe Gly Leu Gly Ser Ala Ile Leu Gly Ser Ala Ala Gly
65                  70                  75                  80
gcg att tta ggg agt tat att ggt aat aag ctt ttc aat aac cct aat   288
Ala Ile Leu Gly Ser Tyr Ile Gly Asn Lys Leu Phe Asn Asn Pro Asn
                85                  90                  95
tac cag caa aac gcc caa cgg acc tac aaa tcc cca caa gct tac caa   336
Tyr Gln Gln Asn Ala Gln Arg Thr Tyr Lys Ser Pro Gln Ala Tyr Gln
            100                 105                 110
cgc tct caa aat tcc ttt tct aaa agt gcg ccc agt gct tca agc atg   384
Arg Ser Gln Asn Ser Phe Ser Lys Ser Ala Pro Ser Ala Ser Ser Met
        115                 120                 125
ggc gga gcg agt aag gga cag agc ggg ttt ttt ggc tct agt agg cct   432
Gly Gly Ala Ser Lys Gly Gln Ser Gly Phe Phe Gly Ser Ser Arg Pro
    130                 135                 140
act agt tca ccg gcg gta agc tct ggg aca agg ggc ttt aac tca       477
Thr Ser Ser Pro Ala Val Ser Ser Gly Thr Arg Gly Phe Asn Ser
145                 150                 155
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<210> 276
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Asn Glu Glu Ile Gln Lys Leu Ile Lys Glu Glu Glu Ala Lys Ile Asp
        35                  40                  45
Asn Gly Thr Ser Lys Leu Val Gln Pro Asn Asn Gly Gly Ser Asn Glu
    50                  55                  60
Gly Ser Gly Phe Gly Leu Gly Ser Ala Ile Leu Gly Ser Ala Ala Gly
65                  70                  75                  80
Ala Ile Leu Gly Ser Tyr Ile Gly Asn Lys Leu Phe Asn Asn Pro Asn
                85                  90                  95
Tyr Gln Gln Asn Ala Gln Arg Thr Tyr Lys Ser Pro Gln Ala Tyr Gln
            100                 105                 110
Arg Ser Gln Asn Ser Phe Ser Lys Ser Ala Pro Ser Ala Ser Ser Met
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ggg gtg gag att gta ggg ttg gag cat ttg gat aaa gtg att tat tta   96
Gly Val Glu Ile Val Gly Leu Glu His Leu Asp Lys Val Ile Tyr Leu
             20                  25                  30
gat caa gcc ccc ata ggc aaa acc cca cga agc aac cct gcc act tac   144
Asp Gln Ala Pro Ile Gly Lys Thr Pro Arg Ser Asn Pro Ala Thr Tyr
         35                  40                  45
acg gga gtg atg gat gaa atc agg att tta ttt gcc gag caa aaa gaa   192
Thr Gly Val Met Asp Glu Ile Arg Ile Leu Phe Ala Glu Gln Lys Glu
     50                  55                  60
gct aaa att tta ggc tat agt gcg agc cgt ttt agc ttt aat gtt aaa   240
Ala Lys Ile Leu Gly Tyr Ser Ala Ser Arg Phe Ser Phe Asn Val Lys
 65                  70                  75                  80
gga ggg cgg tgc gag aaa tgc caa ggc gat ggg gac att aaa ata gaa   288
Gly Gly Arg Cys Glu Lys Cys Gln Gly Asp Gly Asp Ile Lys Ile Glu
                 85                  90                  95
atg cac ttt ttg cct gat gtg tta gtc caa tgc gat agc tgt aag ggc   336
Met His Phe Leu Pro Asp Val Leu Val Gln Cys Asp Ser Cys Lys Gly
            100                 105                 110
gct aaa tac aac ccc caa act tta gaa atc aag gtg aaa ggc aaa tcc   384
Ala Lys Tyr Asn Pro Gln Thr Leu Glu Ile Lys Val Lys Gly Lys Ser
        115                 120                 125
att gcc gat gtg ttg aac atg agc gtg gaa gag gct tat gaa ttt ttt   432
Ile Ala Asp Val Leu Asn Met Ser Val Glu Glu Ala Tyr Glu Phe Phe
    130                 135                 140
gct aaa ttc cct aaa atc gcc gtg aag tta aaa acg ctt atg gat gtg   480
Ala Lys Phe Pro Lys Ile Ala Val Lys Leu Lys Thr Leu Met Asp Val
145                 150                 155                 160
ggc tta ggc tat atc act tta ggg caa aac gct acg act tta agt ggg   528
Gly Leu Gly Tyr Ile Thr Leu Gly Gln Asn Ala Thr Thr Leu Ser Gly
                165                 170                 175
ggg gag gct caa agg atc aaa tta gct aaa gaa ttg agt aaa aaa gac   576
Gly Glu Ala Gln Arg Ile Lys Leu Ala Lys Glu Leu Ser Lys Lys Asp
            180                 185                 190
aca ggc aaa acc ctt tat att tta gat gag cct act acc ggt ttg cat   624
Thr Gly Lys Thr Leu Tyr Ile Leu Asp Glu Pro Thr Thr Gly Leu His
        195                 200                 205
ttt gaa gac gtg aat cat ctt tta caa gtc ttg cat tct tta gtg gcg   672
Phe Glu Asp Val Asn His Leu Leu Gln Val Leu His Ser Leu Val Ala
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             20                  25                  30
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Asp Gln Ala Pro Ile Gly Lys Thr Pro Arg Ser Asn Pro Ala Thr Tyr
        35                  40                  45
Thr Gly Val Met Asp Glu Ile Arg Ile Leu Phe Ala Glu Gln Lys Glu
    50                  55                  60
Ala Lys Ile Leu Gly Tyr Ser Ala Ser Arg Phe Ser Phe Asn Val Lys
65                  70                  75                  80
Gly Gly Arg Cys Glu Lys Cys Gln Gly Asp Gly Asp Ile Lys Ile Glu
                85                  90                  95
Met His Phe Leu Pro Asp Val Leu Val Gln Cys Asp Ser Cys Lys Gly
            100                 105                 110
Ala Lys Tyr Asn Pro Gln Thr Leu Glu Ile Lys Val Lys Gly Lys Ser
        115                 120                 125
Ile Ala Asp Val Leu Asn Met Ser Val Glu Glu Ala Tyr Glu Phe Phe
    130                 135                 140
Ala Lys Phe Pro Lys Ile Ala Val Lys Leu Lys Thr Leu Met Asp Val
145                 150                 155                 160
Gly Leu Gly Tyr Ile Thr Leu Gly Gln Asn Ala Thr Thr Leu Ser Gly
                165                 170                 175
Gly Glu Ala Gln Arg Ile Lys Leu Ala Lys Glu Leu Ser Lys Lys Asp
            180                 185                 190
Thr Gly Lys Thr Leu Tyr Ile Leu Asp Glu Pro Thr Thr Gly Leu His
        195                 200                 205
Phe Glu Asp Val Asn His Leu Leu Gln Val Leu His Ser Leu Val Ala
    210                 215                 220
Leu Gly Asn Ser
225
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INTERNATIONAL SEARCH REPORT

International Application No
PCT/IB 00/00603

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12N15/10 C12Q1/68 C07K14/205 C12N15/31 C12N1/19
C12N1/21 G06F17/00 C12N15/86 C07K16/12 A61K48/00
A61K39/106 A61K39/40

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C12N C12Q C07K G06F A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)
EPO-Internal, WPI Data, MEDLINE, CHEM ABS Data, BIOSIS, EMBL

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	JAMES R. HUDSON ET AL.: "The complete set of predicted genes from Saccharomyces cerevisiae in a readily usable form" GENOME RESEARCH, vol. 7, no. 12, December 1997 (1997-12), pages 1169-1173, XP002127444 the whole document --- -/--	1-43

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search
27 September 2000

Date of mailing of the international search report
11. 10. 00

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Authorized officer
Montero Lopez, B

Form PCT/ISA/210 (second sheet) (July 1992)

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 97 37044 A (ASTRA AKTIEBOLAG) 9 October 1997 (1997-10-09) page 2, line 11 - line 25 page 3, line 12 -page 16, line 15 page 16, line 21 -page 18, line 10 page 33, line 33 -page 34, line 14 page 64, line 22 - line 30	1-3, 7-10, 14-20, 25,26, 30-38, 42,43
Y	WO 98 26072 A (ELI LILLY AND COMPANY) 18 June 1998 (1998-06-18) page 2, line 1 - line 25 page 8, line 10 -page 9, line 2	1,2,5, 7-9,12, 14-19, 22,25, 28, 30-37, 40,42,43
Y	EP 0 786 519 A (HUMAN GENOME SCIENCES, INC.) 30 July 1997 (1997-07-30) page 5, line 41 -page 7, line 7	1,2,4, 7-9,11, 14-19, 21,25, 27, 30-37, 39,42,43
Y	BARTEL ET AL: "A PROTEIN LINKAGE MAP OF ESCHERICHIA COLI BACTERIOPHAGE T7" NATURE GENETICS,US,NEW YORK, NY, vol. 12, no. 12, January 1996 (1996-01), pages 72-77, XP002119798 ISSN: 1061-4036 the whole document	1,2,6-9, 13-19, 23-25, 28-37, 41-43
A	MICHELINE FROMONT-RACINE ET AL.: "Toward a functional analysis of the yeast genome through exhaustive two-hybrid screens" NATURE GENETICS, vol. 16, July 1997 (1997-07), pages 277-282, XP002100296 the whole document	1-43

-/--

INTERNATIONAL SEARCH REPORT

International Application No
PCT/IB 00/00603

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	ROBERT M FREDERCKSON: "Macromolecular matchmaking: advances in two-hybrid and related technologies" CURRENT OPINION IN BIOTECHNOLOGY, vol. 9, no. 1, February 1998 (1998-02), pages 90-96, XP002127445 abstract page 90, left-hand column, paragraph 2 -right-hand column, paragraph 1 page 93, right-hand column, paragraph 2 -page 94, right-hand column, paragraph 1	1-43
A	WO 96 32503 A (THE GENERAL HOSPITAL CORPORATION) 17 October 1996 (1996-10-17) page 4, line 10 -page 7, line 23 page 18, line 28 -page 20, line 33 page 28, line 28 - line 34 page 29, line 14 -page 30, line 16 page 38, line 29 -page 39, line 25 page 43, line 34 -page 45, line 9 page 57, line 18 -page 62, line 4 page 78, line 19 -page 79, line 4	1-43
A	JEAN-F. TOMB ET AL. : "The complete genome sequence of the gastric pathogen Helicobacter pylori" NATURE, vol. 388, 7 August 1997 (1997-08-07), pages 539-547, XP002062106 LONDON GB cited in the application table 2	44-47, 55-58, 76,77, 79-87
X	-& DATABASE EMBL 'Online! Accession number 025047, 1 January 1998 (1998-01-01) XP002148640 the whole document	59-75, 83-87

INTERNATIONAL SEARCH REPORT

International application No.
PCT/IB 00/00603

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

1-43, 53, 54, 79, 80 and partially 44-47, 51, 55-57, 81-87 (inventions 1, 30, 32 and 33)

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☒ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-43

Method for producing a collection of recombinant cell clones usable for two-hybrid systems using genomic DNA from a prokaryotic micro-organism; collection of cell clones so produced; use thereof in yeast two-hybrid systems, kit therefore and recombinant diploid yeast cell so obtained.

2. Claims: Partially 44-47, 51, 55-77, 81-87

Set of two polynucleotide and fragments thereof encoding polypeptide HP0047 of the left column of table I and polynucleotides and fragments thereof encoding interacting ORFs HP0047, HP0048 and HP0695 of the right column of table I; set of two corresponding polypeptides, protein-protein interaction and corresponding complex; computable readable medium having stored such interaction; use of such interacting polypeptides for identifying "selecting interacting domains SID" and SID of SEQ ID NO:68, 70, 72 of Table II and encoding polynucleotides of SEQ ID NO:67, 69, 71 of Table III and homologs thereof; uses thereof as primer or probe; vectors and host cells comprising the same; uses thereof for producing the polypeptides and polypeptides so obtained; uses of the polypeptides in screening assays for for identifying agents capable of modulating such protein-protein interaction; kit therefore and modulator agent so obtained; use of the polypeptides for the modulation of Helicobacter pylori's protein interaction; use for the production of antibodies and antibody so obtained; pharmaceutical compositions comprising any of the above mentioned polynucleotides, polypeptides, vectors, host cells, modulators and antibodies.

3. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0061 of the left column of table I and polypeptides HP0066, HP0978, and HP1409 of the right column of Table I; SID of SEQ ID NO:82, 84 and 86 of Table II and encoding polynucleotides of SEQ ID NO:81, 83 and 85 of Table III

4. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0064 of the left column of table I and polypeptide HP0063 of the right column of Table I; SID of SEQ ID NO:88 of Table II and encoding polynucleotide of SEQ ID NO:87 of Table III

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

5. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0066 of the left column of table I and polypeptide HP0066 of the right column of Table I; SID of SEQ ID NO:76 of Table II and encoding polynucleotide of SEQ ID NO:75 of Table III

6. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0067 of the left column of table I and polypeptides HP0069, HP0609, HP0768, HP0770 and HP0956 of the right column of Table I; SID of SEQ ID NO:196, 198, 200, 202 and 204 of Table II and encoding polynucleotides of SEQ ID NO:195, 197, 199, 201 and 203 of Table III

7. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0068 of the left column of table I and polypeptides HP0070 and HP0118 of the right column of Table I; SID of SEQ ID NO:64 and 66 of Table II and encoding polynucleotides of SEQ ID NO:63 and 65 of Table III

8. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0069 of the left column of table I and polypeptide HP0067 of the right column of Table I; SID of SEQ ID NO:74 of Table II and encoding polynucleotide of SEQ ID NO:73 of Table III

9. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0070 of the left column of table I and polypeptides HP0068 and HP0070 of the right column of Table I; SID of SEQ ID NO:262 and 264 of Table II and encoding polynucleotides of SEQ ID NO:261 and 263 of Table III

10. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0071 of the left column of table I and polypeptides HP0278, HP0417, HP0570, HP0775, HP1340 and HP1409 of the right column of Table I; SID of SEQ ID NO:142, 144, 146, 148, 150 and 152 of Table II and encoding polynucleotides of SEQ ID NO:141, 143, 145, 147, 149 and 151 of Table III

11. Claims: Partially 44-47, 51, 55-77, 81-87

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Idem as subject 2 for polypeptide HP0072 of the left column of table I and polypeptide HP1489 of the right column of Table I; SID of SEQ ID NO:256 of Table II and encoding polynucleotide of SEQ ID NO:255 of Table III

12. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0073 of the left column of table I and polypeptides HP0073, HP0232, HP0259, HP0067, HP0232 and HP0705 of the right column of Table I; SID of SEQ ID NO:154, 156, 158, 274, 276 and 278 of Table II and encoding polynucleotides of SEQ ID NO:153, 155, 157, 273, 275 and 277 of Table III

13. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0268 of the left column of table I and polypeptide HP1198 of the right column of Table I; SID of SEQ ID NO:78 of Table II and encoding polynucleotide of SEQ ID NO:77 of Table III

14. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0289 of the left column of table I and polypeptides HP0289, HP0887, HP0922, HP1038, HP1543, HP0610 and HP1355 of the right column of Table I; SID of SEQ ID NO:44, 46, 48, 50, 52, 54, 56, 58, 60 and 62 of Table II and encoding polynucleotides of SEQ ID NO:43, 45, 47, 49, 51, 53, 55, 57 and 61 of Table III

15. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0311 of the left column of table I and polypeptide HP0312 of the right column of Table I; SID of SEQ ID NO:194 of Table II and encoding polynucleotide of SEQ ID NO:193 of Table III

16. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0338 of the left column of table I and polypeptides HP0132 and HP0337 of the right column of Table I; SID of SEQ ID NO:166 and 168 of Table II and encoding polynucleotides of SEQ ID NO:165 and 167 of Table III

17. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0391 of the left column

of table I and polypeptides HP0392 and HP0392 of the right column of Table I; SID of SEQ ID NO:258 and 260 of Table II and encoding polynucleotides of SEQ ID NO:257 and 259 of Table III

18. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0691 of the left column of table I and polypeptides HP0692 and HP1362 of the right column of Table I; SID of SEQ ID NO:266 and 268 of Table II and encoding polynucleotides of SEQ ID NO:265 and 267 of Table III

19. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0697 of the left column of table I and polypeptides HP0012, HP0048, HP0558, HP0599, HP0696, HP0684, HP1037, HP1038, HP1299 and HP1576 of the right column of Table I; SID of SEQ ID NO:222, 224, 226, 228, 230, 232, 234, 236, 238 and 240 of Table II and encoding polynucleotides of SEQ ID NO:221, 223, 225, 227, 229, 231, 233, 235, 237 and 239 of Table III

20. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0776 of the left column of table I and polypeptides HP0067, HP0278, HP1378, and HP1409 of the right column of Table I; SID of SEQ ID NO:214, 216, 218 and 220 of Table II and encoding polynucleotides of SEQ ID NO:213, 215, 217 and 219 of Table III

21. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0797 of the left column of table I and polypeptides HP0289, HP0887, HP1349, HP1377 and HP1409 of the right column of Table I; SID of SEQ ID NO:184, 186, 188, 190 and 192 of Table II and encoding polynucleotides of SEQ ID NO:183, 185, 187, 189 and 191 of Table III

22. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0800 of the left column of table I and polypeptides HP0433, HP0687, HP0800, HP0801, HP0924, HP1267 and HP1460 of the right column of Table I; SID of SEQ ID NO:10, 12, 14, 16, 18, 20 and 22 of Table II and encoding polynucleotides of SEQ ID NO:9, 11, 13, 15, 17, 19 and 21 of Table III

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

23. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0801 of the left column of table I and polypeptides HP0152, HP0800 and HP1513 of the right column of Table I; SID of SEQ ID NO:24, 26, and 28 of Table II and encoding polynucleotides of SEQ ID NO:23, 25 and 27 of Table III

24. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0868 of the left column of table I and polypeptides HP0088, HP0327, HP0869, and HP1142 of the right column of Table I; SID of SEQ ID NO:2, 4, 6 and 8 of Table II and encoding polynucleotides of SEQ ID NO:1, 3, 5 and 7 of Table III

25. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0874 of the left column of table I and polypeptide HP0875 of the right column of Table I; SID of SEQ ID NO:254 of Table II and encoding polynucleotide of SEQ ID NO:253 of Table III

26. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0875 of the left column of table I and polypeptide HP0874 of the right column of Table I; SID of SEQ ID NO:212 of Table II and encoding polynucleotide of SEQ ID NO:211 of Table III

27. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0887 of the left column of table I and polypeptides HP0459, HP0610, HP0699, HP0887, HP1157, HP1460, and HP1464 of the right column of Table I; SID of SEQ ID NO:30, 32, 34, 36, 38, 40, 42, 242, 244, 246 and 248 of Table II and encoding polynucleotides of SEQ ID NO:29, 31, 33, 35, 37, 39, 40, 41, 241, 243, 245 and 247 of Table III

28. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0935 of the left column of table I and polypeptides HP0072, HP0528 and HP0657 of the right column of Table I; SID of SEQ ID NO:160, 162 and 164 of Table II and encoding polynucleotides of SEQ ID NO:159, 161 and 163 of Table III

29. Claims: Partially 44-47, 51, 55-77, 81-87

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Idem as subject 2 for polypeptide HP0978 of the left column of table I and polypeptides HP0979 and HP1583 of the right column of Table I; SID of SEQ ID NO:138 and 140 of Table II and encoding polynucleotides of SEQ ID NO:137 and 139 of Table III

30. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP1032 of the left column of table I and polypeptides HP0643, HP0818, HP1122, HP1198 and HP1316 of the right column of Table I; SID of SEQ ID NO:122, 124, 126, 128 and 130 of Table II and encoding polynucleotides of SEQ ID NO:121, 123, 125, 127 and 129 of Table III

31. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP1067 of the left column of table I and polypeptide HP0392 of the right column of Table I; SID of SEQ ID NO:210 of Table II and encoding polynucleotide of SEQ ID NO:209 of Table III

32. Claims: 53, 54, 79, 80 and partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP1198 of the left column of table I and polypeptides HP0088, HP0268, HP0293, HP0452, HP0705, HP0775, HP0965, HP1032, HP1114, HP1124, HP1198, HP1274, HP1378, HP1411, HP1541 and HP1218 of the right column of Table I; SID of SEQ ID NO:90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 270 and 272 of Table II and encoding polynucleotides of SEQ ID NO:89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 269 and 271 of Table III

33. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP1230 of the left column of table I and polypeptides HP1230 and HP1529 of the right column of Table I; SID of SEQ ID NO:132, 134 and 136 of Table II and encoding polynucleotides of SEQ ID NO:131, 133 and 135 of Table III

34. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP1231 of the left column of table I and polypeptide HP1247 of the right column of Table I; SID of SEQ ID NO:120 of Table II and encoding

polynucleotide of SEQ ID NO:119 of Table III

35. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP1244 of the left column of table I and polypeptides HP0857 and HP1246 of the right column of Table I; SID of SEQ ID NO:206 and 208 of Table II and encoding polynucleotides of SEQ ID NO:205 and 207 of Table III

36. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP1246 of the left column of table I and polypeptides HP0121, HP0326, HP0407, HP0886, HP1035, HP1244 and HP1460 of the right column of Table I; SID of SEQ ID NO:170, 172, 174, 176, 178, 180 and 182 of Table II and encoding polynucleotides of SEQ ID NO:169, 171, 173, 175, 177, 179 and 181 of Table III

37. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP1247 of the left column of table I and polypeptides HP1231 and HP1353 of the right column of Table I; SID of SEQ ID NO:250 and 252 of Table II and encoding polynucleotides of SEQ ID NO:249 and 251 of Table III

38. Claims: 52, 78 and partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP1293 of the left column of table I and polypeptide HP1198 of the right column of Table I; SID of SEQ ID NO:80 of Table II and encoding polynucleotide of SEQ ID NO:79 of Table III

39. Claims: 48 and partially 44-46, 51, 55-57-59, 76, 77, 81, 82, 84-87

Set of two polynucleotides and fragments thereof encoding two Staphylococcus polypeptides; set of two corresponding polypeptides, protein-protein interaction and corresponding complex; computable readable medium having stored such interaction; use of such interacting polypeptides for identifying "selecting interacting domains SID" and polynucleotide encoding SID; uses of the polypeptides in screening assays for for identifying agents capable of modulating such protein-protein interaction; kit therefore and modulator agent so obtained; use of the polypeptides in the preparation of antibodies; antibodies so produced and pharmaceutical compositions comprising any of the above

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

mentioned polypeptides, polynucleotides, modulators or antibodies.

40. Claims: 49 and partially 44-46, 51, 55-57-59, 76, 77, 81, 82, 84-87

Idem as subject 39 for Streptococcus pneumoniae polypeptides and polynucleotides.

41. Claims: 50 and partially 44-46, 51, 55-57-59, 76, 77, 81, 82, 84-87

Idem as subject 39 for Escherichia coli polypeptides and polynucleotides.

42. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 interacting polypeptides not covered by the above mentioned subjects

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Information on patent family members

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